

OM protein - protein search, using SW model						
Run on:	May 18, 2004, 18:0:16 ; Search time 22 Seconds (without alignments) 370.768 Million cell updates/sec					
Title:	US-09-887-593A-2					
Perfect score:	862					
Sequence:	1 MHGRSVIHTIVASLILHLS.....ADGELESMGESARYNFTPGK 158					
Scoring table:	BIO3M62					
Gapop 10.0 , Gapext 0.5						
Searched:	389414 seqs, 51625971 residues					
Total number of hits satisfying chosen parameters:	389414					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
Database :	Issued Patents AA:*					
1:	/cggn2_6/podata/2/iaa/5A-COMB_Pep:*					
2:	/cggn2_6/podata/2/iaa/5B-COMB_Pep:*					
3:	/cggn2_6/podata/2/iaa/6A-COMB_Pep:*					
4:	/cggn2_6/podata/2/iaa/6B-COMB_Pep:*					
5:	/cggn2_6/podata/2/iaa/PCIIUS-COMB_Pep:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query	Length	DB	ID	Description
1	862	100.0	158	3	US-09-374-135-2	Sequence 2, Appli
2	260	30.2	115	3	US-09-374-135-3	Sequence 3, Appli
3	238.5	27.7	1013	2	US-09-866-650-3	Sequence 3, Appli
4	238.5	27.7	1013	2	US-09-021-287-3	Sequence 3, Appli
5	238.5	27.7	1013	2	US-09-400-473-3	Sequence 3, Appli
6	233.5	27.1	1013	2	US-08-866-650-5	Sequence 5, Appli
7	233.5	27.1	1013	2	US-09-021-287-5	Sequence 5, Appli
8	233.5	27.1	1013	3	US-08-991-408-2	Sequence 2, Appli
9	233.5	27.1	1013	3	US-09-240-473-5	Sequence 5, Appli
10	233.5	27.1	1013	4	US-09-432-973-2	Sequence 2, Appli
11	233.5	27.1	1013	4	US-09-285-385C-20	Sequence 20, Appli
12	232.5	27.0	591	3	US-08-991-408-4	Sequence 4, Appli
13	232.5	27.0	591	4	US-09-332-973-4	Sequence 4, Appli
14	228.5	26.5	1012	4	US-09-285-385C-4	Sequence 4, Appli
15	227	26.3	1015	4	US-09-285-385C-2	Sequence 2, Appli
16	226	26.2	901	3	US-08-936-135-22	Sequence 22, Appli
17	226	26.2	901	4	US-09-439-711C-22	Sequence 20, Appli
18	226	26.2	906	3	US-08-936-135-24	Sequence 24, Appli
19	226	26.2	906	4	US-09-439-711C-24	Sequence 24, Appli
20	226	26.2	909	3	US-08-936-135-8	Sequence 8, Appli
21	226	26.2	909	3	US-08-936-135-10	Sequence 10, Appli
22	226	26.2	909	4	US-09-439-711C-8	Sequence 8, Appli
23	226	26.2	909	4	US-09-439-711C-10	Sequence 10, Appli
24	226	26.2	914	3	US-08-936-135-12	Sequence 12, Appli
25	226	26.2	914	4	US-09-439-711C-12	Sequence 12, Appli
26	226	26.2	926	3	US-08-936-135-14	Sequence 14, Appli
27	226	26.2	926	4	US-09-439-711C-14	Sequence 14, Appli

ALIGNMENTS

48	24.0	26.2	26.2	931	3	US-09-936-135-16	Sequence 16, Appli
49	24.0	26.2	26.2	931	4	US-09-439-711C-16	Sequence 16, Appli
50	22.5	26.1	925	4	US-09-116-473-2	Sequence 2, Appli	
51	22.4	26.0	909	3	US-09-936-135-18	Sequence 18, Appli	
52	22.4	26.0	909	4	US-09-439-711C-18	Sequence 18, Appli	
53	22.4	26.0	925	3	US-08-936-135-20	Sequence 20, Appli	
54	22.4	26.0	926	4	US-09-439-711C-20	Sequence 20, Appli	
55	22.4	26.0	931	4	US-09-583-638-4	Sequence 4, Appli	
56	22.5	25.8	102	3	US-09-374-135-7	Sequence 7, Appli	
57	22.5	25.8	3623	4	US-09-341-461-2	Sequence 2, Appli	
58	22.2	25.8	923	4	US-09-439-711C-2	Sequence 2, Appli	
59	22.1	25.6	923	4	US-09-583-638-2	Sequence 2, Appli	
60	22.0	25.6	986	4	US-09-285-385C-19	Sequence 19, Appli	
61	21.9	25.5	986	4	US-09-872-577-4	Sequence 4, Appli	
62	21.9	25.5	985	4	US-09-850-048A-4	Sequence 4, Appli	
63	21.7	25.2	921	4	US-09-439-711C-4	Sequence 4, Appli	
64	21.7	25.2	922	4	US-09-116-473-4	Sequence 4, Appli	
65	21.6	25.1	923	3	US-08-936-135-5	Sequence 6, Appli	

APPLICANT: Leong, Kahan
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Saffran, Douglas C.
 APPLICANT: Jakobovits, Aya
 TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND FILED BY PROSTATE AND BLADDER CANCER CELLS
 FILE REFERENCE: 1703-017.US1
 CURRENT APPLICATION NUMBER: US/09/374,135
 PRIOR APPLICATION NUMBER: 60/095,982
 PRIOR FILING DATE: 1998-08-10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 3
 LENGTH: 115
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-09-874-135-3
 Query Match 30.2%; Score 260; DB 3; Length 115;
 Best Local Similarity 43.5%; Pred. No. 1-1e-24;
 Matches 50; Conservative 20; Mismatches 37; Indels 8; Gaps 2;
 QY 52 IFTSPNPKSPYPPRECIYIEAPROCIELYDEKYSIEPSW-----ECKFDHIEVR 104
 Db 1 IFTSPNPKSPYPPRECIYIEAPROCIELYDEKYSIEPSW-----ECKFDHIEVR 60
 QY 105 DGGPGSPPIGLRGCGQKQPP-VIKSSGFLWKFADGELESMGSFARYNFPGK 158
 Db 61 DGRGPGSPPIGLRGCGQKQPP-VIKSSGFLWKFADGELESMGSFARYNFPGK 115
 RESULT 3
 US-08-866-650-3
 Sequence 3, Application US/08866650
 ; Patent No. 5939321
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuiko
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021,287
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37194
 REFERENCE/DOCKET NUMBER: 960296.93839
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-021-287-3
 Query Match 27.7%; Score 238.5; DB 2; Length 1013;
 Best Local Similarity 39.3%; Pred. No. 1-2e-20;
 Matches 42; Conservative 25; Mismatches 39; Indels 1; Gaps 1;
 QY 47 HAGGGIFFSPNPKSPYPPRECIYIEAPROCIELYDEKYSIEPSWCKFDHIEVR 106
 Db 779 HSPSGLITSPNWPDKYPKRECTWVISAIPGHRTLAINE-FEVEQHOCAYDHLIEFDG 837
 QY 107 PFGSPPIGLRGCGQKQPP-VIKSSGFLWKFADGELESMGSFARYN 153
 Db 838 ETEKSPPIGLRGCGQKQPP-VIKSSGFLWKFADGELESMGSFARYNFPGK 884
 RESULT 4
 US-09-021-287-3
 Sequence 3, Application US/09021287
 ; Patent No. 598117
 GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuiko
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/021,287
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37194
 REFERENCE/DOCKET NUMBER: 960296.93839
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1013 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-021-287-3
 Query Match 27.7%; Score 238.5; DB 2; Length 1013;
 Best Local Similarity 39.3%; Pred. No. 1-2e-20;
 Matches 42; Conservative 25; Mismatches 39; Indels 1; Gaps 1;
 QY 47 HAGGGIFFSPNPKSPYPPRECIYIEAPROCIELYDEKYSIEPSWCKFDHIEVR 106
 Db 779 HSPSGLITSPNWPDKYPKRECTWVISAIPGHRTLAINE-FEVEQHOCAYDHLIEFDG 837
 QY 107 PFGSPPIGLRGCGQKQPP-VIKSSGFLWKFADGELESMGSFARYN 153
 Db 838 ETEKSPPIGLRGCGQKQPP-VIKSSGFLWKFADGELESMGSFARYNFPGK 884
 RESULT 5
 US-09-473-3
 Sequence 3, Application US/09240473

Patent No. 6,297,011

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,473
FILING DATE: 09/09/2001
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1013 amino acids
TYPE: amino acid
TOPeLOGY: linear

MOLECULE TYPE: protein

US-08-866-650-5

Query Match 27.1%; Score 233.5; DB 2; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4.9e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

QY 47 HAEGGIFTSPNPKSKPPDKPDRCTYIIEAAPQCITYFDEKYSIERSWECKFDHIEVRDG 106
Db 779 HSPSGIITSPPNPKSKPPDKPDRCTWESATPCHRIRKAFSE-FEIEHQBCAYDHIEVRDG 837

QY 107 PFGFSPIIGRCGQQNPVVKSSGRITWIKFADGILMSGFSARYN 153
Db 838 ETEKSPPIGLRGKNDPLVATGNKMFVRFVSDASVORKGQFATHS 884

RESULT 6

US-08-866-650-5

Sequence 5, Application US/09021287
Patent No. 5981717

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021-287
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/866, 650
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839
TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1013 amino acids
TYPE: amino acid
TOPeology: linear

; MOLECULE TYPE: protein
; US-09-021-287-5

Query Match 27.1%; Score 233.5; DB 2; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4_9e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEKGIFSPNPKSPKVPPDRECIVYLEAPROCYELYDEKYSIESPWECKFDHIEYRDG 106

Db 779 HSPGLITSPNPKSPRKECTWEISATPGHRIKLAFASE-FEIEQHQECAYDHLEVFDG 837

Qy 107 PFGFSPIGRFGQQNPKPVISSESGRELWIKFADGELESMSMGFSARYN 153

Db 838 ETEKSPILGRIGCNKIPDPPLVATGNKMFVRFVSDASVQRKGFOATHS 884

RESULT 8
US-08-991-408-2

; Sequence 2, Application US/08991408

; Patent No. 67008017

; GENERAL INFORMATION:

; APPLICANT: ARLETH, ANTHONY J.

; APPLICANT: WILLETTE, ROBERT N.

; APPLICANT: ELSOURBAGY, NABIL A.

; APPLICANT: LI, XIAOTONG

; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE

; NUMBER OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/991,408

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 60/034,471

; FILING DATE: 02-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: ATG-50038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1013 amino acids

; TYPE: amino acid

; STRANDBEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-991-408-2

; MOLECULE TYPE: protein
; US-09-240-473-2

Query Match 27.1%; Score 233.5; DB 3; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4_9e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEKGIFSPNPKSPKVPPDRECIVYLEAPROCYELYDEKYSIESPWECKFDHIEYRDG 106

Db 779 HSPGLITSPNPKSPRKECTWEISATPGHRIKLAFASE-FEIEQHQECAYDHLEVFDG 837

Qy 107 PFGFSPIGRFGQQNPKPVISSESGRELWIKFADGELESMSMGFSARYN 153

Db 838 ETEKSPILGRIGCNKIPDPPLVATGNKMFVRFVSDASVQRKGFOATHS 884

RESULT 10
US-09-132-473-2

; Sequence 2, Application US/09432473

; Patent No. 6365715

; GENERAL INFORMATION:

; APPLICANT: ARLETH, ANTHONY J.

; APPLICANT: WILLETTE, ROBERT N.

; APPLICANT: ELSOURBAGY, NABIL A.

; APPLICANT: LI, XIAOTONG

; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN

; FILE REFERENCE: ATG-50038-D1

; CURRENT APPLICATION NUMBER: US/09/432,473

; CURRENT FILING DATE: 1999-11-01

; EARLIER APPLICATION NUMBER: 08/991,408

; EARLIER FILING DATE: 1997-12-16

Query Match 27.1%; Score 233.5; DB 3; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4_9e-20;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEKGIFSPNPKSPKVPPDRECIVYLEAPROCYELYDEKYSIESPWECKFDHIEYRDG 106

Db 779 HSPGLITSPNPKSPRKECTWEISATPGHRIKLAFASE-FEIEQHQECAYDHLEVFDG 837

Qy 107 PFGFSPIGRFGQQNPKPVISSESGRELWIKFADGELESMSMGFSARYN 153

Db 107 PFGFSPIGRFGQQNPKPVISSESGRELWIKFADGELESMSMGFSARYN 153

; EARLIER APPLICATION NUMBER: 60/034,471
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-432-473-2

Query Match Similarity 27.1%; Score 233.5; DB 4; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4.9e-20; Indels 1; Gaps 1;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEGGIFTSPNYPKYPDIRECTIVTEAAPROCTIELYDFEKSISIIPSWECKFDHIEVRDG 106
Db 779 HSPSGLITSPNWPDKPSRKECTWEISATPGRHRIKAFSE-FETEQHREAYDHLFEDG 837

Qy 107 PFGESPITGRFCGQONPPVTKSSGRFLWIKFFADGELESMGFSARYN 153
Db 838 ETEKSPILGRLCGNKIPDPLVATGNKMFVRFVSDASVORKGFOATHS 884

RESULT 11
US-09-285-385C-20
; Sequence 20, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960226.96111
; CURRENT APPLICATION NUMBER: US/09/285, 385C
; CURRENT FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-285-385C-20

Query Match Similarity 27.1%; Score 233.5; DB 4; Length 1013;
Best Local Similarity 40.2%; Pred. No. 4.9e-20; Indels 1; Gaps 1;
Matches 43; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 47 HAEGGIFTSPNYPKYPDIRECTIVTEAAPROCTIELYDFEKSISIIPSWECKFDHIEVRDG 106
Db 779 HSPSGLITSPNWPDKPSRKECTWEISATPGRHRIKAFSE-FETEQHREAYDHLFEDG 837

Qy 107 PFGESPITGRFCGQONPPVTKSSGRFLWIKFFADGELESMGFSARYN 153
Db 838 ETEKSPILGRLCGNKIPDPLVATGNKMFVRFVSDASVORKGFOATHS 884

RESULT 12
US-08-991-408-4
; Sequence 4, Application US/08991408
; Patent No. 6003017
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: ARLETH, ROBERT N.
; APPLICANT: WILLETTE, ROBERT N.
; APPLICANT: LI, XIAOTONG
; APPLICANT: ELSOURBAGY, NABIL A.
; APPLICANT: ELSOURBAGY, NABIL A.
; APPLICANT: LI, XIAOTONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

RESULT 13
US-09-432-473-4
; Sequence 4, Application US/09432473
; Patent No. 6365715
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: WILLETTE, ROBERT N.
; APPLICANT: LI, XIAOTONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
; FILE REFERENCE: ATG-50038-D1
; CURRENT APPLICATION NUMBER: US/09/432,473
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 08/991,408
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: 60/034,471
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-432-473-4

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-408-4

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-408-4

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-408-4

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Query Match 27.0%; Score 232.5; DB 4; Length 591;
Best Local Similarity 40.2%; Pred. No. 3.1e-20; Indels 1; Ga.
Matches 43; Conservative 23; Mismatches 40; Indels 1; Ga.

RESULT 14
US-09-285-385C-4
; Sequence 4, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296_96111
; CURRENT APPLICATION NUMBER: US/09/285, 385C
; CURRENT FILING DATE: 1999-04-02
; PRIORITY NUMBER: 60/111873
; PRIORITY FILING DATE: 1998-12-11
; PRIORITY APPLICATION NUMBER: 60/080550
; PRIORITY FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: PRT
; ORGANISM: mouse
; US-09-285-385C-4

RESULT 15
US-09-285-385C-2
; Sequence 2, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296_96111
; CURRENT APPLICATION NUMBER: US/09/285, 385C
; CURRENT FILING DATE: 1999-04-02
; PRIORITY NUMBER: 60/111873
; PRIORITY FILING DATE: 1998-12-11
; PRIORITY APPLICATION NUMBER: 60/080550
; PRIORITY FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: human
; US-09-285-385C-2

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Query Match          26.3%; Score 227; DB 4; length 1015;
Best Local Similarity 37.7%; Pred. No. 3.2e-19;
Matches 43; Conservative 23; Mismatches 46; Index 2; Gaps 2;
QY          37 KSVQCGITWIKHAEGGFTTSPNPXPSKPPDRCTYIEAAPQCTYEDERKSYIESWEC 96
Do          772 KEAGCAHKISSVGETL-ASPNNPDKPSRRECTWNISSTAGHRVKLTNF-PEIEQHQC 829
QY          97 KFDHIEVRDGPFGPSPIIGRFGCQQWPPVVKSSGRFLWIKFADGELEMSPA 150
Db          830 AVYDHEWYTDGPDSSLAPILGRFCGSKBDPPTAVGSSMELRFYSDASVORKGFOA 883

```


AC ABB79587;

XX

DT 21-OCT-2002 (first entry)

XX Human CUB domain-containing protein 39362.

XX CUB domain protein; 39362; human; antiarteriosclerotic; cardiant;

XX cerebroprotective; hypotensive; antiarthematic; antiarthritic;

XX anti-allergic; neuroprotective; cytostatic; antithyroid; vasotropic;

XX antiasthmatic; antidiabetic; nephrotropic; antiparkinsonian;

XX antiinflammatory; gene therapy.

OS Homo sapiens.

XX

PH

FT Key

FT Domain

FT 1. .344 /note= "predicted N-terminal extracellular domain"

FT 1. .23 /label= "Signal_peptide"

FT 23. .25 /note= "predicted protein kinase C phosphorylation site"

FT 24. .533 /label= "Mature_protein"

FT 24. .27 /note= "predicted cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT 27. .29 /note= "predicted protein kinase C phosphorylation site"

FT 31. .34 /note= "predicted casein kinase II phosphorylation site"

FT 35. .37 /note= "predicted protein kinase C phosphorylation site"

FT 41. .152 /note= "predicted CUB domain"

FT 50. .55 /note= "predicted protein kinase C phosphorylation site"

FT 129. .131 /note= "predicted protein kinase C phosphorylation site"

FT 149. .151 /note= "predicted protein kinase C phosphorylation site"

FT 172. .284 /note= "predicted N-myristoylation site"

FT 177. .182 /note= "predicted N-myristoylation site"

FT 195. .198 /note= "predicted casein kinase II phosphorylation site"

FT 241. .244 /note= "predicted casein kinase II phosphorylation site"

FT 274. .279 /note= "predicted casein kinase II phosphorylation site"

FT 285. .289 /note= "predicted N-myristoylation site"

FT 290. .328 /note= "predicted casein kinase II phosphorylation site"

FT Domain

FT Modified-site

FT /note= "predicted low density lipoprotein receptor class A domain"

FT 306. .309 /note= "predicted N-glycosylation site"

FT 313. .318 /note= "predicted N-myristoylation site"

FT 329. .332 /note= "predicted N-myristoylation site"

FT Modified-site

FT 333. .336 /note= "predicted casein kinase II phosphorylation site"

FT 340. .343 /note= "predicted N-glycosylation site"

FT Modified-site

FT 341. .351 /note= "predicted prokaryotic membrane lipoprotein lipid attachment site"

FT Modified-site

FT 343. .348 /note= "predicted N-myristoylation site"

FT Domain

FT /note= "predicted transmembrane domain"

FT Domain

FT 364. .533 /note= "predicted C-terminal cytoplasmic domain"

FT 377. .380 /note= "predicted casein kinase II phosphorylation site"

FT 397. .399 /note= "predicted protein kinase C phosphorylation site"

FT 400. .405 /note= "predicted N-myristoylation site"

FT 421. .424 /note= "predicted cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT 424. .426 /note= "predicted protein kinase C phosphorylation site"

FT 434. .439 /note= "predicted N-myristoylation site"

FT 439. .441 /note= "predicted protein kinase C phosphorylation site"

FT 442. .447 /note= "predicted protein kinase C phosphorylation site"

FT 446. .449 /note= "predicted N-myristoylation site"

FT 448. .451 /note= "predicted N-myristoylation site"

FT 448. .450 /note= "predicted casein kinase II phosphorylation site"

FT 481. .484 /note= "predicted protein kinase C phosphorylation site"

FT 502. .504 /note= "predicted N-glycosylation site"

FT 506. .509 /note= "predicted protein kinase C phosphorylation site"

FT 522. .525 /note= "predicted casein kinase II phosphorylation site"

FT 529. .532 /note= "predicted N-glycosylation site"

FT 530. .532 /note= "predicted protein kinase C phosphorylation site"

FT 531. .533 /note= "predicted microbody C-targeting signal"

FT Region

XX

PD 01-AUG-2002.

XX

PR 08-JAN-2002; 2002WO-US000275.

XX

PR 08-JAN-2001; 2001US-0260286P.

XX

PA (MTI-) MILLENNIUM PHARM INC.

XX

DR N-P5DB; ABN84415.

XX

PS WPI; 2002-590825/63.

XX

CC The present sequence is the protein sequence of 39362, a novel human CUB domain-containing protein family member. The invention provides isolated

CC 39362 proteins, fusion proteins, antigenic peptides and anti-39362

CC antibodies. It also provides isolated 39362 nucleic acid molecules,

CC antisense nucleic acid molecules, recombinant expression vectors, host

CC cells, and non-human transgenic animals, a method for identifying a

CC compound that binds 39362, a method for modulating 39362 polypeptide

CC activity, a method of inhibiting aberrant activity of a 39362-expressing

CC cell using a peptide, phosphopeptide, small organic molecule or molecule,

CC and a method of treating or preventing a disorder characterised by

CC aberrant activity or a 39362-expressing cell, especially a cardiovascular

cell, by administering a compound that modulates the activity or expression of 39362 nucleic acid. 39362 proteins are useful in treating 39362-mediated 1 -related diseases, such as conditions involving cardiovascular disorders (e.g. atherosclerosis, myocardial infarction, aneurysm, stroke, hypertension), inflammatory disorders (e.g. rheumatoid arthritis, allergy, multiple sclerosis), and cellular proliferation or differentiation (e.g. cancer, Grave's disease, ischaemic disease). They may also be used in diagnosing, preventing or treating asthma, emphysema, chronic pulmonary disease, nephropathy, diabetes, hyperlipidaemia, infections (e.g. bacterial, viral, parasitic), hepatic injury, Parkinson's disease, or Alzheimer's disease, anxiety or cardiovascular conditions associated with interventional procedures, such as restenosis following angioplasty. 39362 proteins, protein homologues, antibodies and nucleic acids are also useful as screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays, forensic biology, monitoring clinical trials, and pharmacogenetics), and methods of treatment (e.g. therapeutic and prophylactic)

XX
SQ Sequence 533 AA:

Query Match 98.7%; Score 851; DB 5; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.7e-88; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHGRSLVHTVASSLILHSGATKKGTEKQTTSETQKSVQCGTWIKHAGEGIFTSNYP 60
1 MIGRSVLVHTVASSLILHSGATKKGTEKQTTSETQKSVQCGTWIKHAGEGIFTSNYP 60

QY 61 KYPDPDRBCIYIEAAPROCTELYDEKYSIERSWECKFDHIEVRDQPGFGSPICLPRFCGQ 120
61 KYPDPDRBCIYIEAAPROCTELYDEKYSIERSWECKFDHIEVRDQPGFGSPICLPRFCGQ 120

Db 121 QNPVVKSSGPIFLWIKFADGELESMGFSARVNFTP 156
121 QNPVVKSSGPIFLWIKFADGELESMGFSARVNFTP 156

Db 121 QNPVVKSSGPIFLWIKFADGELESMGFSARVNFTP 156

RESULT 4
ADC42850

ID ADC42850 standard; protein; 525 AA.

XX
AC ADC42850;
XX
DT 18-DEC-2003 (first entry)

XX
DE REMAP protein #10.

XX
KW Cytosatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;

KW Antiallergic; Antidiabetic; REMAP; Pathogenesis.

OS Homo sapiens.

XX
PN WO2003027228-A2.

XX
PD 03-APR-2003.

XX
PP 16-JUL-2002; 2002WO-TU5022833.

XX
PR 17-JUL-2001; 2001US-0306020P.

PR 27-JUL-2001; 2001US-0308179P.

PR 02-AUG-2001; 2001US-0309702P.

PR 10-AUG-2001; 2001US-0311476P.

PR 10-AUG-2001; 2001US-0311531P.

PR 10-AUG-2001; 2001US-0311738P.

PR 24-AUG-2001; 2001US-0314790P.

PR 31-AUG-2001; 2001US-0316639P.

PR 07-SEP-2001; 2001US-0317996P.

XX
PA (INCY-) INCYTE GENOMICS INC.

XX
PI Lal PG, Honchell CD, Forbythe IJ, Walia NK, Tang TY, Borowsky ML;

PI Barroso I, Yue H, Warren BA, Duggan BM, Tran B, Li JX;

PI Lee EA, Baughn MR, Gorvad AE;

PI

PI Richardson TW, Elliott VS, Zebardadian Y, Tran UK, Yao MG;
PI Peterson DP, Luo W, Lehr-Mason PM;
XX
WPI: 2003-421156/39.

XX
PT New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating or preventing disorders associated with aberrant REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or stroke.

XX
PS Claim 1; SEQ ID NO 10; 115P; English.

XX
CC The present invention relates to an isolated polypeptide. The polypeptides and polynucleotides are useful in diagnosis, treating and preventing disorders associated with aberrant expression of REMAP, such as cell proliferative, autoimmune/inflammatory, renal, neurological, cardiovascular, metabolic, developmental, endocrine, muscle, gastrointestinal, lipid metabolism or transport disorders, and viral infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acids and amino acid sequences of REMAP, in facilitating drug discovery process, and in investigating the pathogenesis of diseases or medical conditions. Expression and purification were achieved using bacterial or virus-based expression systems. The present sequence represents an REMAP protein of the invention.

XX
SQ Sequence 525 AA:

Query Match 93.0%; Score 802; DB 7; Length 525;
Best Local Similarity 99.3%; Pred. No. 7e-83; Matches 146; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 0 YVASLILHSGATKKGTEKQTTSETQKSVQCGTWIKHAGEGIFTSNYP 69
1 0 YVASLILHSGATKKGTEKQTTSETQKSVQCGTWIKHAGEGIFTSNYP 69

Db 2 WASLILHSGATKKGTEKQTTSETQKSVQCGTWIKHAGEGIFTSNYP 121
2 WASLILHSGATKKGTEKQTTSETQKSVQCGTWIKHAGEGIFTSNYP 121

QY 70 YTEAAPROCTELYDEKYSIERSWECKFDHIEVRDQPGFGSPICLPRFCGQONPPVIKS 129
62 YTEAAPROCTELYDEKYSIERSWECKFDHIEVRDQPGFGSPICLPRFCGQONPPVIKS 129

Db 130 GRFLWIKFFADGELESMGFSARVNFTP 156
130 GRFLWIKFFADGELESMGFSARVNFTP 156

QY 122 GRFLWIKFFADGELESMGFSARVNFTP 148
Db 122 GRFLWIKFFADGELESMGFSARVNFTP 148

RESULT 5
ABB10345

ID ABB10345 standard; protein; 130 AA.

XX
AC ABB10345;
XX
DT 10-JAN-2002 (first entry)

XX
DE Human cDNA SEQ ID NO: 653.

XX
KW Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.

XX
OS Homo sapiens.

XX
FN WO200154474-A2.

XX
PR 02-AUG-2001.

XX
PR 17-JAN-2001; 2001WO-US001349.

XX
PR 31-JAN-2000; 2000US-017905P.

PR 04-FEB-2000; 2000US-018062P.

PR 24-FEB-2000; 2000US-018466P.

PR 02-MAR-2000; 2000US-018635P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-NOV-2000; 2000US-0249317P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249397P.
 PR 17-NOV-2000; 2000US-0249399P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-025030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX DR WPI; 2001-46558/50.
 XX DR N-PSDB; AAS31604.
 PT Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition.
 XX PA Claim 11; SEQ ID NO 116; 542pp; English.
 CC The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS3157-AAS31654) and genomic sequences encoding for those proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. acquired immunodeficiency, AIDS), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAS19892-AAS19969 represent the novel human calcium-binding proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 141 AA;

Query Match 55.6%; Score 479; DB 4; Length 141;
 Best Local Similarity 66.1%; Pred. No. 1; 4e-46;
 Matches 80; Conservative 21; Mismatches 20; Indels 0; Gaps 0;

QY 3B SWQCGTWTKHAGGIFTSPNYSKPPDRCEIVIEAAMPQTYIHYDEBKISIEPSWCK 97
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 9 AQQCGIWIWRTSNGHFPASPNYPPDYPKECTYLEAPRQTYIHYDEBKISIEPSWCK 97
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 98 PDIIEVRUGPFGSPRPGFCGQONPVYKTSERFLWIKFEDGELSMGRVARYNTPG 157
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 69 FDIIEVRUGPFGSPRPGFCGQONPVYKTSERFLWIKFEDGELSMGRVARYNTPG 128
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 158 K 158
 Db 129 K 129

AB11868
 ID ABB11868 standard; peptide; 352 AA.
 XX
 AC ABB11868;
 XX DT 11-JAN-2002 (first entry)
 XX DE Human secreted protein homologue, SEQ ID NO:2238.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasorotic; cardiant; virucide; antibacterial; fungicidal; vulnerary; antiulcer.
 XX OS Homo sapiens.
 XX PN WO200157188-A2.
 XX PD 09-AUG-2001.
 XX PR 05-FEB-2001; 2001WO-US003800.
 XX PR 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI; 2001-457740/49.
 XX DR N-PSDB; ABA09112.
 PT Human Proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.
 XX PA Claim 20; Page 268; 1963PP; English.
 CC sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09514 represent nucleic acids encoding them. The invention relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic application. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haemopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 XX polypeptide of the invention.

SQ Sequence 352 AA;

Query Match 54.5%; Score 470; DB 4; Length 352;
 Best Local Similarity 54.9%; Pred. No. 5.1e-45; Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVLHT--VASYLILHISGATKKGGTSETOKSVQCGTWKHAEGGIFTSPNPKVSP 63
 Db 28 SVLKVLILTVLWVEGIAVAKQTQDGFSPLIDRQVSP 87
 QY 64 PDRECYTIEAAPROCTYLEDEKYSIESPWECKEDHIEYRDGRGFSPIGRGQQNP 123
 ID 88 PNKECYIILFAAPROCTYLEDEHYYIEPSFCREDHLEVRDGPRGFSPSLIDRQVSP 147
 Db 148 PLIRSTGGRFWMIKFSDEELEGGLGRAKYSFIP 180

RESULT 9

ADC2852 ID ADC2852 standard; protein; 487 AA.

AC *AC

XX

DT DT

XX

DE DE

XX

KW KW

OS OS

XX

XX

PN PN

XX

PD PD

XX

PF PF

XX

PR PR

XX

(INCY-) INCYTE GENOMICS INC.

Lal PG, Honchell CD, Foraythe IJ, Walia NK, Tang TY, Borowsky ML;

Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;

Lee EA, Baughn MR, Gorv AE, Duggan BM, Tran B, Li JX;

Richardson TM, Elliott VS, ZeharJadian Y, Tran UK, Yao MG;

Peterson DP, Luo W, Lehr-Mason PM;

WPI; 2003-421156/39.

PT New human receptors and membrane-associated proteins (REMAP), useful for

PT diagnosing, treating or preventing disorders associated with aberrant
 PT REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or
 PT stroke.

XX Claim 1; SEQ ID NO 12, 115pp; English.

The present invention relates to an isolated polypeptide. The
 CC polypeptides and polymers are useful in diagnosing, treating and
 preventing disorders associated with aberrant expression of REMAP, such
 CC as cell proliferative, autoimmune/inflammatory, renal, neurological,
 CC cardiovascular, metabolic, developmental, endocrine, muscle,
 CC gastrointestinal, lipid metabolism or transport disorders, and viral
 CC infections. These are also useful in assessing the effects of exogenous
 CC compounds on the expression of nucleic acids and amino acid sequences of
 REMAP, in facilitating drug discovery processes, and in investigating the
 CC pathogenesis of diseases or medical conditions. Expression and
 CC purification were achieved using bacterial or virus-based expression
 CC systems. The present sequence represents an REMAP protein of the
 CC invention.

SQ Sequence 487 AA;

Query Match 54.5%; Score 470; DB 7; Length 487;
 Best Local Similarity 54.9%; Pred. No. 8e-45; Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

QY 6 SVLHT--VASYLILHISGATKKGGTSETOKSVQCGTWKHAEGGIFTSPNPKVSP 63
 Db 8 SVLKVLILTVLWVEGIAVAKQTQDGFSPLIDRQVSP 67

QY 64 PDRECYTIEAAPROCTYLEDEKYSIESPWECKEDHIEYRDGRGFSPIGRGQQNP 123

Db 68 PNKECYIILFAAPROCTYLEDEHYYIEPSFCREDHLEVRDGPRGFSPSLIDRQVSP 127

QY 124 PVKSSGRFWMIKFSDEELEGGLGRAKYSFIP 156

Db 128 PLIRSTGGRFWMIKFSDEELEGGLGRAKYSFIP 160

RESULT 10

AAM93946

ID AAM93946 standard; protein; 525 AA.

AC AC

XX

DT DT

XX

DE DE

XX

KW KW

OS OS

XX

Homo sapiens.

XX

WO2003027228-A2.

XX

PD PD

XX

03-APR-2003.

XX

16-JUL-2002; 2002W0-US022833.

XX

17-JUL-2001; 2001US-03060205.

XX

27-JUL-2001; 2001US-0308179P.

XX

02-AUG-2001; 2001US-0309702P.

XX

10-AUG-2001; 2001US-0311476P.

XX

10-AUG-2001; 2001US-0311552P.

XX

PR 24-AUG-2001; 2001US-0311718P.

XX

PR 31-AUG-2001; 2001US-0316639P.

XX

PR 07-SEP-2001; 2001US-0317996P.

XX

PA PA

(INCY-) INCYTE GENOMICS INC.

XX

PT

PI Lal PG, Honchell CD, Foraythe IJ, Walia NK, Tang TY, Borowsky ML;

PI Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;

PI Lee EA, Baughn MR, Gorv AE, Duggan BM, Tran B, Li JX;

PI Richardson TM, Elliott VS, ZeharJadian Y, Tran UK, Yao MG;

PI Peterson DP, Luo W, Lehr-Mason PM;

DR WPI; 2003-421156/39.

XX

DR N-PSDB; AAK94910.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use

in genetic manipulation.

Db	68	PNKECIVITIEAARPROCTELTFDEHYIEPSFECRFDFHLEVRDGFPGSPFLDRYCGVKS P	FT	Modified-site	475. .479
Qy	124	PVIKSSERFLWIKFFADGELESMGFSARYNFP 156	FT	/label= N-glycosylation site	479. .483
Db	128	PLURSTGRFMWIKFSSDEELBEGLGFRAXSFIP 160	FT	/label= cAMP + cGMP-dependant protein kinase	
RESULT	12		XX	phosphorylation site	
XX	AAB47296	standard; protein; 525 AA.	XX		
XX	ID	AAB47296	AC		
XX	XX		AC	AAB47296;	
XX	XX		XX	22-AUG-2001 (first entry)	
DE	PRO4401	polypeptide.	XX		
XX	XX		XX		
KW	PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte; PRO1199; PRO1556; PRO4901; PRO1028; inhibition; stimulation; infiltration; mononuclear cell; eosinophil; erythema multiforme; polymorphonuclear neutrophil; PMN; antibody; immune-related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease; systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma; autoimmune thrombocytopenia; thyroditis; diabetes mellitus; allergy; immune-mediated renal disease; demyelination; central nervous system; peripheral nervous system; idiopathic demyelinating polyneuropathy; Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia; chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis; granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity; inflammatory bowel disease; gluten-sensitive enteropathy; urticaria; Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis; psoriasis; atopic dermatitis; hypersensitivity pneumonitis; graft rejection; graft-versus-host disease.	XX			
OS	Homo sapiens.		XX		
XX	XX		XX		
Key	Location/Qualifiers		XX		
Peptide	1..22		XX		
PT	/label= Signal peptide		XX		
PT	Modified-site	22..28	XX		
Protein	/label= N-myristoylation site	23..525	XX		
PT	Modified-site	32..38	XX		
PT	/label= N-myristoylation site	54..60	XX		
PT	Modified-site	186..192	XX		
PT	Modified-site	279..285	XX		
PT	/label= N-myristoylation site	311..315	XX		
PT	Modified-site	318..324	XX		
PT	Modified-site	348..369	XX		
Domain	/label= Transmembrane domain	348..354	XX		
PT	Modified-site	352..358	XX		
PT	Modified-site	385..389	XX		
PT	Modified-site	426..430	XX		
PT	Modified-site	441..447	XX		
PT	Modified-site	453..457	XX		
PT	/label= N-glycosylation site		XX		
Qy	6	SVHLH--VASLILHLSGATKKGEMKQPTSETQKSVQGTWRAEGLIFSPNYPKSP 63	Qy	Query	54.5%; Score 470; DB 4; Length 525;
Db	8	SVLKLITLVVREGIAVAKQDQGNGIKHAPATQCGIWRTSNGCHFASPNYPQSP 67	Db	Best Local Similarity 54.9%; Pred. No. 8.8e-45; Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;	
Qy	64	PDRRCIVITIEAARPROCTELTFDEHYIEPSFECRFDFHLEVRDGFPGSPFLDRYCGVKS P	Qy	64 PDRRCIVITIEAARPROCTELTFDEHYIEPSFECRFDFHLEVRDGFPGSPFLDRYCGVKS P	

Db	6 8	PNKECYIILEAPRQRIELTFDHEYIERSFCRDLEVRDGFPGFSPLIDRCGVKSP	127	PR 20-DEC-1999; 99WO-US030911. PR 20-DEC-1999; 99WO-US030999. PR 22-DEC-1999; 99WO-US030720. PR 30-DEC-1999; 99WO-US031243. PR 30-DEC-1999; 99WO-US031274. PR 05-JAN-2000; 2000WO-US00219. PR 06-JAN-2000; 2000WO-US00277. PR 06-JAN-2000; 2000WO-US003565. PR 11-FEB-2000; 2000WO-US00411. PR 18-FEB-2000; 2000WO-US004342. PR 18-FEB-2000; 2000WO-US004414. PR 22-FEB-2000; 2000WO-US005841. PR 10-MAR-2000; 2000WO-US006319. PR 15-MAR-2000; 2000WO-US06884. PR 20-MAR-2000; 2000WO-US00737. PR 21-MAR-2000; 2000WO-US007532. PR 30-MAR-2000; 2000WO-US008439. PR 17-MAY-2000; 2000WO-US013705. PR 22-MAY-2000; 2000WO-US014042. PR 30-MAY-2000; 2000WO-US014941. PR 02-JUN-2000; 2000WO-US015264. PR 28-JUL-2000; 2000WO-US020710. PR 11-AUG-2000; 2000WO-US022031. PR 23-AUG-2000; 2000WO-US023522. PR 24-AUG-2000; 2000WO-US02328. PR 08-NOV-2000; 2000WO-US030952. PR 10-NOV-2000; 2000WO-US030873. PR 01-DEC-2000; 2000WO-US034678. PR 20-DEC-2000; 2000US-00747259. PR 20-DEC-2000; 2000WO-US034956. PR 28-FEB-2001; 2001US-00794498. PR 28-FEB-2001; 2001WO-US005220. PR 01-MAR-2001; 2001WO-US006666. PR 09-MAR-2001; 2001US-00802706. PR 14-MAR-2001; 2001US-00805689. PR 22-MAR-2001; 2001US-00816744. PR 05-APR-2001; 2001US-00828366. PR 10-MAY-2001; 2001US-00854208. PR 10-MAY-2001; 2001US-00854280. PR 18-MAY-2001; 2001US-00860216. PR 25-MAY-2001; 2001US-00866028. PR 25-MAY-2001; 2001US-00866034. PR 25-MAY-2001; 2001WO-US011992. PR 01-JUN-2001; 2001US-00872035. PR 01-JUN-2001; 2001WO-US017800. PR 05-JUN-2001; 2001US-00874503. PR 14-JUN-2001; 2001US-00882636. PR 19-JUN-2001; 2001US-00886342. PR 20-JUN-2001; 2001WO-US019692. PR 21-JUN-2001; 2001US-00887879. PR 22-JUN-2001; 2001WO-US020116. PR 29-JUN-2001; 2001WO-US021666. PR 09-JUL-2001; 2001WO-US021735. PR 18-JUL-2001; 2001US-00908927. PR 06-AUG-2001; 2001US-00924419. PR 09-AUG-2001; 2001US-00927796. PR 15-AUG-2001; 2001US-00931836. PR 19-DEC-2001; 2001US-00028072.
QY	124	PKVKSRRFWIKFEPADGELESMGISARYNTP	156	
Db	128	PLIRSTGRFMWIKFSSDEELLEGFLGRAKYSP	160	
RESULT 13				
ID	AB017672	standard; protein; 525 AA.		
XX	AC	AB017672;		
XX	XX	26-AUG-2003 (first entry)		
DE	DE	Novel human secreted and transmembrane protein PRO4401.		
XX	XX	Human; secreted and transmembrane protein; PRO; antiinflammatory; anti-arteriosclerotic; cardiot; anti-infertility; anti-HIV; cytostatic; anti-diabetic; gene therapy; tumour necrosis factor (TNF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.		
OS	OS	Homo sapiens.		
XX	XX	US2003032156-A1.		
PN	XX	US2003032156-A1.		
PD	PD	13-FEB-2003.		
XX	XX	06-MAY-2002; 2002US-00140474.		
XX	XX	31-MAR-1997; 97WO-US005230.		
PR	PR	12-JUN-1998; 98WO-US012456.		
PR	PR	14-JUL-1998; 98WO-US014552.		
PR	PR	28-AUG-1998; 98WO-US017888.		
PR	PR	10-SEP-1998; 98WO-US018824.		
PR	PR	14-SEP-1998; 98WO-US019093.		
PR	PR	14-SEP-1998; 98WO-US019094.		
PR	PR	16-SEP-1998; 98WO-US019177.		
PR	PR	17-SEP-1998; 98WO-US019437.		
PR	PR	17-OCT-1998; 98WO-US021141.		
PR	PR	29-OCT-1998; 98WO-US022991.		
PR	PR	29-OCT-1998; 98WO-US022992.		
PR	PR	01-DEC-1998; 98WO-US024555.		
PR	PR	03-DEC-1998; 98WO-US024555.		
PR	PR	05-JAN-1999; 99WO-US000106.		
PR	PR	08-MAY-1999; 99WO-US005028.		
PR	PR	10-MAR-1999; 99WO-US005190.		
PR	PR	20-APR-1999; 99WO-US008615.		
PR	PR	14-MAY-1999; 99WO-US010733.		
PR	PR	03-JUN-1999; 99WO-US01222.		
PR	PR	01-SEP-1999; 99WO-US020111.		
PR	PR	08-SEP-1999; 99WO-US020194.		
PR	PR	13-SEP-1999; 99WO-US02084.		
PR	PR	15-SEP-1999; 99WO-US021547.		
PR	PR	15-SEP-1999; 99WO-US021030.		
PR	PR	05-OCT-1999; 99WO-US02089.		
PR	PR	29-NOV-1999; 99WO-US028214.		
PR	PR	30-NOV-1999; 99WO-US028313.		
PR	PR	01-DEC-1999; 99WO-US028301.		
PR	PR	01-DEC-1999; 99WO-US028634.		
PR	PR	02-DEC-1999; 99WO-US028551.		
PR	PR	02-DEC-1999; 99WO-US028564.		
PR	PR	02-DEC-1999; 99WO-US028565.		
PR	PR	16-DEC-1999; 99WO-US030095.		
PA	PA	(GERTH) GENENTECH INC.		
XX	XX	Baker KP, Berestini M, Deforge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith N, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPT; 2003-341980/32.		
DR	DR	N_PSDB; ACD23909.		

PT New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.

XX
 PS Claim 12; Fig 114; 660pp; English.

CC The invention describes an isolated nucleic acid (I) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (I) is used to
 CC detect PRO polypeptide, link a biactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 CC the proliferation or differentiation of cells or gene expression,
 CC stimulate the release of proteoglycans, stimulate the release of cytokine
 CC from peripheral blood mononuclear cells, inhibit the binding of R-peptide
 CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
 acid and polypeptide encoded by it, are useful for treating inflammatory
 diseases, organ failure, atherosclerosis, cardiac injury, infertility,
 birth defects, premature aging, acquired immunodeficiency syndrome
 (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosomes and gene mapping, and in generating
 CC antisense RNA or DNA. The nucleic acids are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
 CC This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide

XX Sequence 525 AA;

Query Match 54.5%; Score 470; DB 6; Length 525;
 Best Local Similarity 54.9%; Pred. No. 8.8e-45; Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
 QY 6 SVLHITVANLILHISGAKKGTKQTETQKSVQCGWTKHAEGLTSPNPKV 63
 Db 8 SVLKVLLITVIVVEGIVAKTQDGTGQIGKHPATQGQWRTSNGHHPSP 67
 QY 64 PDRECYITIAAPRCQELYFDEKVISIEPSWECKEDHIEVRDGPFGSPSP 123
 Db 68 PNKECTYILLLAPRQIETLDEHYKIEPSPCRDHLIEVRDGPFGSPFLIDR 127
 QY 124 PVIKSSGRFWIKFFADGELESMGISARYVFTP 156
 Db 128 PLIRSTGRFWWIKFSSDEELIGLFRAKYSP 160

RESULT 14
 ABU80926 ID ABU80926 standard; protein; 525 AA.
 XX AC ABU80926;
 XX DT 23-JUN-2003 (first entry)
 DE Human PRO polypeptide #57.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac; antidiabetic; anorectic; vulnerable; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic.
 XX OS Homo sapiens.
 XX US2003004311-A1.
 XX 02-JAN-2003.
 XX

PF	19-DEC-2001; 2001US-00028072.
XX	18-JUN-1997; 97US-0049911P.
PR	26-AUG-1997; 97US-005674P.
PR	17-SEP-1997; 97US-0059115P.
PR	17-SEP-1997; 97US-0059115P.
PR	18-SEP-1997; 97US-0059363P.
PR	19-SEP-1997; 97US-0059352P.
PR	19-SEP-1997; 97US-0059388P.
PR	24-SEP-1997; 97US-0059336P.
PR	17-OCT-1997; 97US-0062250P.
PR	17-OCT-1997; 97US-0062285P.
PR	17-OCT-1997; 97US-0062287P.
PR	17-OCT-1997; 97US-006327P.
PR	24-OCT-1997; 97US-006329P.
PR	24-OCT-1997; 97US-0063550P.
PR	24-OCT-1997; 97US-0063612P.
PR	24-OCT-1997; 97US-006327P.
PR	27-OCT-1997; 97US-006327P.
PR	27-OCT-1997; 97US-006327P.
PR	28-OCT-1997; 97US-0063550P.
PR	28-OCT-1997; 97US-0063561P.
PR	29-OCT-1997; 97US-0063304P.
PR	29-OCT-1997; 97US-0063733P.
PR	29-OCT-1997; 97US-0063735P.
PR	29-OCT-1997; 97US-0063738P.
PR	03-NOV-1997; 97US-0064809P.
PR	07-NOV-1997; 97US-0064809P.
PR	12-NOV-1997; 97US-0063186P.
PR	17-NOV-1997; 97US-005846P.
PR	21-NOV-1997; 97US-0063154P.
PR	24-NOV-1997; 97US-0063453P.
PR	24-NOV-1997; 97US-006511P.
PR	24-NOV-1997; 97US-0065170P.
PR	11-DEC-1997; 97US-006312P.
PR	11-DEC-1997; 97US-0059278P.
PR	11-DEC-1997; 97US-005934P.
PR	16-DEC-1997; 97US-0063694P.
PR	23-JAN-1998; 98US-0073232P.
PR	04-FEB-1998; 98US-0073612P.
PR	09-FEB-1998; 98US-0074086P.
PR	09-FEB-1998; 98US-0074902P.
PR	12-MAR-1998; 98US-0077791P.
PR	20-MAR-1998; 98US-0078910P.
PR	25-MAR-1998; 98US-0079294P.
PR	27-MAR-1998; 98US-017963P.
PR	27-MAR-1998; 98US-007928P.
PR	31-MAR-1998; 98US-0080165P.
PR	98US-0080165P.
PR	98US-0012456.
PR	14-JUL-1998; 98US-0014552.
PR	28-AUG-1998; 98US-0017888.
PR	10-SEP-1998; 98US-0018824.
PR	14-SEP-1998; 98US-0019093.
PR	14-SEP-1998; 98US-0019094.
PR	14-SEP-1998; 98US-0019177.
PR	16-SEP-1998; 98US-0019130.
PR	17-SEP-1998; 98US-0019437.
PR	07-OCT-1998; 98US-0021141.
PR	29-OCT-1998; 98US-0022991.
PR	29-OCT-1998; 98US-0022992.
PR	20-NOV-1998; 98US-0024855.
PR	01-DEC-1998; 98US-0025108.
PR	05-JAN-1999; 99US-0001016.
PR	08-MAR-1999; 99US-0005028.
PR	10-MAR-1999; 99US-0015190.
PR	20-APR-1999; 99US-008615.
PR	14-MAY-1999; 99US-0010733.
PR	02-JUN-1999; 99US-0012252.
PR	01-SEP-1999; 99US-0020111.

PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 10-MAR-2000; 2000WO-US005811.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007332.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014494.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUN-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US02231.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US04956.
 PR 28-FEB-2001; 2001US-0079498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001WO-US006666.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-0082366.
 PR 10-MAY-2001; 2001US-00854200.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-0086034.
 PR 01-OCT-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-0088342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00897879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Berezini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-33204/031.
 DR N-PSDB; ACA03659.

CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for for
 CC identifying agonists or antagonists. The PRO polypeptides are useful for
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
 CC human blood, for stimulating the proliferation or differentiation of
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,
 CC in chromosome and gene mapping, in the generation of antisense RNA and
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic
 CC animals or knock-out animals, for the genetic analysis of individuals with
 CC genetic disorders, and in gene therapy. ABU6570-ABU6684 represent the
 CC human PRO polypeptides of the invention. Note: The sequence data for this
 CC patent was obtained in electronic format directly from the USPTO web site
 CC at seqdata.uspto.gov/psipubIDentry.html

SQ Sequence 525 AA;

Query	Match	Score	DB	Length
QY	6 SVLHIV-VASLILHSGATKGKTEQQTSETQKSYQCGTWKHAEGGIFTSPNYSKP	54.5%	6	525;
Db	8 SVLKVLITLVNEGIAVAKQHGDGNIGKHPAQCGTWKHAEGGIFTSPNYSKP	54.5%	6	525;
QY	64 PDRECYIIEAPQOELYDEKYSIEPSNECKFDHIEVRDGPFQFSPTGRFCQONP	54.5%	64	525;
Db	68 PNKECTYLEAPRQIETDEHYVIEPSRECFLHLEVRDGPFQFSPLIDRYCCVSP	54.5%	68	525;
QY	124 PVKSGGRFLWIKFEDGELELSMGSSARVYKFTP	54.5%	124	156;
Db	128 PLIRSGTRFMWIKFSSDEBELGLGFRAKYSIP	54.5%	128	160;

Search completed: May 18, 2004, 18:22:24
 Job time : 60 secs

PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
 PT typing, and in chromosome identification.

XX Claim 12: Fig 114; 660pp; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO

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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:19:46 ; Search time 39 Seconds

(without alignments) 1278.253 Million cell updates/sec

Title: US-09-887-593A-2
Perfect score: 852
Sequence: 1 MHGRGSVHLHVASLILHLS..... ADGELPSMGFSARYNFTPGK 158

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25;*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 851 98.7 533 4 Q8TD05 Q8tdf5 homo sapien

2 843 97.8 533 4 Q8EW85 Q8ew85 homo sapien

3 818 94.9 533 11 Q8RA17 Q8ra17 mus musculus

4 818 94.9 533 11 Q8DX39 Q8dx39 mus musculus

5 814 94.4 533 11 Q8C4S3 Q8c4s3 mus musculus

6 802 93.0 156 4 Q8TD04 Q8tdf4 homo sapien

7 690 80.0 156 4 Q8ND78 Q8nd78 homo sapien

8 494 57.3 466 11 Q8CCM2 Q8ccm2 mus musculus

9 470 54.5 525 4 Q8NC67 Q8nc67 homo sapien

10 468 54.3 491 4 Q7Z381 Q7z381 homo sapien

11 465 53.9 444 11 Q8E4Q8 Q8c4q8 mus musculus

12 53.9 525 11 Q8BN76 Q8bn76 mus musculus

13 341 39.6 451 4 Q8nd51 Q8nd51 homo sapien

14 260 30.2 321 5 Q61B49 Q61b49 caenorhabditis

15 250 29.0 677 5 Q9VYCT Q9vyct drosophila

16 238.5 27.7 1013 11 Q62381 Q62381 mus musculus

RESULT 1

ID Q8TD05 PRELIMINARY, PRT: 533 AA.

AC Q8TD05; DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Neuroplilin and tolloid like-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE:Retina;
RX MEDLINE:21940629; PubMed=11943477;
RA Stohr H., Berger C., Frohlich S., Weber B.H.;
RT "A novel gene encoding a putative transmembrane protein with two extracellular CUB domains and a low-density lipoprotein class A module: isolation of alternatively spliced isoforms in retina and brain.";
RT Gene 296:223-231(2002).
RT Gene 296:223-231(2002).
RT CC !- SIMILARITY: CONTAINS 2 CUB DOMAINS.
RT EMBL; AF448338; AAM18026.1; -.
RT GENBANK; HGNC:13823; NETO1.
RT InterPro; IPR000959; CUB.
RT InterPro; IPR002172; LDL_receptor_A.
RT PFAM; PF00431; CUB; 2.
RT PFAM; PF00057; IgL_recept_a; 1.
RT SMART; SM00042; CUB; 2.
RT SMART; SM00192; LDL; 1.
RT PROSITE; PS01180; CUB; 2.
RT PROSITE; PS0068; LDL; 2; 1.
RT PROSITE; PS0068; LDL; 2; 1.
SQ SEQUENCE 533 AA; 60218 MW; 5B3EB7BBB8031BL CRC64;

Query Match 98.7%; Score 851; DB 4; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.1e-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL and mouse CUB sequences.";
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R;
 RA Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX PubMed=12810072;
 RA Michishita M., Ikeda T., Nakashiba T., Ogawa M., Tashiro K., Honjo T.,
 RA Doi K., Itohara S., Endo S.;
 RT "A novel gene, Brcl, encoding CUB and LDA domains is expressed in
 restricted areas of mouse brain.";
 RL Biochem. Biophys. Res. Commun. 306:680-685 (2003).
 EMBL BC051145; AAH51145.1; -;
 EMBL AX138900; AAN38318.1; -;
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000859; CUB.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00057; IgL_recept_a; 1.
 SMART; SM00442; CUB; 2.
 SMART; SM00192; LDA; 1.
 PROSITE; PS01180; CUB; 2.
 PROSITE; PS50068; LDRA_2; 1.
 KW transmembrane.
 SQ 533 AA; 60248 MW; 04319A6F9458CB3D CRC64;
 Query Match 94.4%; Score 814; DB 11; Length 533;
 Best Local Similarity 93.6%; Pred. No. 1 4e-81;
 Matches 146; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 RT 147; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 OY 1 MTHGRSVHIVHLVSLILHLSGATKGKGKQTKSETQKSQVCGWTKHAEGLITSPNYS 60
 1 MYGRSLFHITASLILHLSGATKGKGKQTKITPETQKSQVCGWTKHAEGLITSPNYS 60
 Db 61 KYPDPRECIVYLEAAPROCYIEFDEKYSIESWECKEDHIEVRDGPRGFSPIGRCQ 120
 61 KYPDPRECIVYLEAAPROCYIEFDEKYSIESWECKEDHIEVRDGPRGFSPIGRCQ 120
 QY 61 KYPDPRECIVYLEAAPROCYIEFDEKYSIESWECKEDHIEVRDGPRGFSPIGRCQ 120
 Db 121 QNPFPVIKSSGRFLWIKKFADGELESMGFSARYNFTP 156
 121 QNPFPVIKSSGRFLWIKKFADGELESMGFSARYNFTP 156
 Db 121 QNPFPVIKSSGRFLWIKKFADGELESMGFSARYNFTP 156
 RESULT 5
 O8C4S3 PRELIMINARY; PRT; 533 AA.
 ID O8C4S3
 AC Q8C4S3;
 AC Q8C4S3; 2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Neuropilin and toll-like-1.
 DB Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 DR SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=2190629; PubMed=11943477;
 RA Strohr H., Berger C., Frohlich S., Weber B. H.;
 RT "A novel gene encoding a putative transmembrane protein with two
 extracellular CUB domains and a low-density lipoprotein class A
 module; isolation of alternatively spliced isoforms in retina and
 brain.";
 RT Gene 286:223-231(2002).
 RL Gene 286:223-231(2002).
 CC 100% SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AF448339; KAM18027.1; -.
 DR InterPro; IPR000859; CUB.
 DR Pfam; PF00431; CUB; 1.
 DR SMART; SM00442; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR RNP
 RN SEQUENCE FROM N.A.
 RN STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The RANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.;"
 RL Nature 420:563-573 (2002).
 EMBL; AK081325; BRC38196.1; -.
 MGD; MGI:2180216; Neto1.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR002172; IgL_recept_a.

RESULT 7

Q8ND78 PRELIMINARY; PRT; 500 AA.

ID Q8ND78; TISSUE=brain; Created)

AC DT 01-OCT-2002 (T-EMBLrel. 22, last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)

DR DE Hypothetical protein (Fragment).

GN DKFZ0547B197.

OS Homo sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=brain;

RA Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.

DR EMBL; ALB34354; CAD9019.1; -.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR002172; LDL_receptor_A.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00431; Idl_recept_a; 1.

DR SMART; SMO0042; CUB; 2.

DR SMART; SMO0192; CUB; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS50068; LDLRA_2; 1.

DR PROSITE; PS50068; LDLRA_2; 1.

DR NON_TER 1

FT NON_TER 1

FT SEQUENCE 500 AA; 56708 MW; 313628B650C49F08 CRC64;

DR Best Local Similarity 80.0%; Score 690; DB 4; Length 500;

DR Beet Local Similarity 100.0%; Pred. No. 7.4e-68; Length 500;

DR Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR Hypothetical protein.

QY 34 ETQKSYVQGCTWIKHAGGIFTSPNYSKYPDRECYIEAARPROCILEYDEKYSIERS 93

Db 1 ETOKSYVQGCTWIKHAGGIFTSPNYSKYPDRECYIEAARPROCILEYDEKYSIERS 60

RESULT 8

Q8NC67 PRELIMINARY; PRT; 525 AA.

ID Q8NC67; TISSUE=brain; Created)

AC DT 01-OCT-2002 (T-EMBLrel. 22, last sequence update)

AC DT 01-OCT-2002 (T-EMBLrel. 25, last annotation update)

AC DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)

DR DE Hypothetical protein FLJ90456.

OS Homo sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=9606;

RN [1] SEQUENCE FROM N.A.

RC Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Itoh S., Kawai-Hirai Y., Saito K., Yamamoto J., Oka T., Nakamura Y., Kojima S., Nagahashi K., Masuno Y., Ono T., Okano K., Yoshioka Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Niimiyama K., "NEDO human cDNA sequencing project.", Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

DR CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.

DR EMBL; AK074937; BAC11303.1; -.

DR Genew; HGNC:14644; NETO2.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR002172; LDL_receptor_A.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00057; Idl_recept_a; 1.

DR SMART; SMO0042; CUB; 2.

DR SMART; SMO0192; CUB; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS50068; LDLRA_2; 1.

DR PROSITE; PS50068; LDLRA_2; 1.

DR NON_TER 1

FT NON_TER 1

FT SEQUENCE 525 AA; 59392 MW; EA6F98C3A8B220EA_CRC64;

DR Best Local Similarity 54.5%; Score 470; DB 4; Length 525;

DR Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

DR Hypothetical protein.

QY 6 SVLHI--VSLVLIILHISGATKGKGTEHQTSITQKSYVQGCTWIKHAGGIFTSPNYSKYP 63

Db 8 SVLKVLIITVLVEGIAVQAKTQDGQNGNIGKIPANTQGIVWRTSNGHASPQNYPSD 67

QY 64 PDRECYIEAARPROCILEYDEKYSIERSWCKFDEIYEVDRDGPFGFSPITGRFCGQONP 123

Db 68 PNKCECYILEAPQRQIETFDEHYIIEPSFCRFDHLEVRDGPFGFSPILIDRYCGKSP 127

DR EMBL; AK032510; BAC27902.1; -.

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibebewam C., DR SMART; SW00042; CUB; 2.
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., DR SMART; SW00192; LDDA; 1.
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., DR PROSITE; PS01180; CUB; 2.
 RA Lasko P., Lei Y., Levitsky A.T., Li J., Li Z., Liang Y., Lin X., DR PROSITE; PS01189; LDDA; 1; 1.
 RA Liu X., Mattei B., McIntosh T.C., McLoud M.P., McPherson D., DR PROSITE; PS50688; LDDA; 2; 1.
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mohrefi A., DR PROSITE; PS50689; LDDA; 2; 1.
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L., DR PROSITE; PS50690; LDDA; 2; 1.
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., DR PROSITE; PS50691; LDDA; 1; 1.
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., DR PROSITE; PS50692; LDDA; 2; 1.
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., DR PROSITE; PS50693; LDDA; 2; 1.
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., DR PROSITE; PS50694; LDDA; 2; 1.
 RA Spier E., Spradling A.C., Stopleton M., Strong R., Sun E., DR PROSITE; PS50695; LDDA; 2; 1.
 RA Svilskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., DR PROSITE; PS50696; LDDA; 2; 1.
 RA Wang Z.-Y., Wasserman D.A., Wainstock G.M., Weissbach J., DR PROSITE; PS50697; LDDA; 2; 1.
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., DR PROSITE; PS50698; LDDA; 2; 1.
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., DR PROSITE; PS50699; LDDA; 2; 1.
 RA Zheng X.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., DR PROSITE; PS50700; LDDA; 2; 1.
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., DR PROSITE; PS50701; LDDA; 2; 1.
 RA "The genome sequence of *Drosophila melanogaster*.", DR PROSITE; PS50702; LDDA; 2; 1.
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., DR SMART; SW00043; CUB; 2.
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., DR SMART; SW00044; CUB; 2.
 RA Carlson J.J., Aan H., Baldwin D., Banzon J., Beeson K.Y., Busan D.A., DR SMART; SW00045; CUB; 2.
 RA Carlson J.W., Center M., Chapple M., Davenport L.B., Dietz S.M., DR SMART; SW00046; CUB; 2.
 RA Dodson K., Dorsett V., Doupe L.E., Doyle C., Dresnick D., Farfan D., DR SMART; SW00047; CUB; 2.
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A., DR SMART; SW00048; CUB; 2.
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., DR SMART; SW00049; CUB; 2.
 RA Ibebewam C., Jalali M., Kruse D., Li P., Mattei B., Mohrefi A., DR SMART; SW00050; CUB; 2.
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Munoo J., DR SMART; SW00051; CUB; 2.
 RA Pacieb J., Paragis V., Park S., Patel S., Pfeiffer B., DR SMART; SW00052; CUB; 2.
 RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., DR SMART; SW00053; CUB; 2.
 RA Stapleton M., Strong R., Svilskas R., Tector C., Tyler D., DR SMART; SW00054; CUB; 2.
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., DR SMART; SW00055; CUB; 2.
 RT "Sequencing of *Drosophila melanogaster* genome.", DR SMART; SW00056; CUB; 2.
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., DR SMART; SW00057; CUB; 2.
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., DR SMART; SW00058; CUB; 2.
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., DR SMART; SW00059; CUB; 2.
 RA Clamp M., Drysdale R., Ermert D., Frise E., de Grey A., Harris N., DR SMART; SW00060; CUB; 2.
 RA Kronmiller B., MathHall B., Millburn G., Richter J., Russo S., DR SMART; SW00061; CUB; 2.
 RA Searle S.M.J., Smith E., Shu S., Smutnicki F., Whitfield E., DR SMART; SW00062; CUB; 2.
 RA Ashburner M., Gehalt W.M., Rubin G.M., Munagall C.J., Lewis S.E.; DR SMART; SW00063; CUB; 2.
 RT "Annotation of *Drosophila melanogaster* genome.", DR SMART; SW00064; CUB; 2.
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., DR SMART; SW00065; CUB; 2.
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase; DR SMART; SW00066; CUB; 2.
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., DR SMART; SW00067; CUB; 2.
 RA Champé M., Chavez M., Dorsett V., Dresnick D., Farfan D., Frise E., DR SMART; SW00068; CUB; 2.
 RA George R., Gonzalez M., Guarini H., Kronmiller B., Li P., Liao G., DR SMART; SW00069; CUB; 2.
 RA Miranda A., Mungall C.J., Nunoo J., Pacieb J., Paragis V., Park S., DR SMART; SW00070; CUB; 2.
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., DR SMART; SW00071; CUB; 2.
 RA Celniker S.; DR SMART; SW00072; CUB; 2.
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC ! SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL; AE03492; AAC48276.2; --.
 DR EMBL; AV070839; AAC48461.1; --.
 DR FlyBase; FBgn0052635; CG32635.
 DR InterPro; IPR00089; CUB.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR Pfam; PRO0431; CUB; 2.
 DR Pfam; PRO0431; CUB; 2.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:16:31 ; Search time 17 Seconds

Sequence: (without alignments) 483.946 Million cell updates/sec

Title: US-09-887-593A-2

Perfect score: 862

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 & Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	232.5	27.0	914	1 NRP1 CHICK
2	227	26.3	707	1 NRP1_XENLA
3	227	26.3	931	1 NRP2_MOUSE
4	225	26.1	925	1 NRP2_RAT
5	224	26.0	931	1 NRP2_HUMAN
6	224	25.6	991	1 NRP1_MOUSE
7	221	25.6	923	1 NRP1_HUMAN
8	220.5	25.6	986	1 NRP1_HUMAN
9	217.5	25.2	1022	1 TLD_BRAKE
10	217	25.2	1057	1 TLD_DROME
11	217	25.2	922	1 NRP1_RAT
12	215	25.1	923	1 CSM1_MOUSE
13	215	24.9	639	1 BMPH_STRPU
14	201.5	23.4	449	1 PCO1_HUMAN
15	198.5	23.0	928	1 NRP1_XENLA
16	194.5	22.6	468	1 PCO1_MOUSE
17	194.5	22.6	468	1 PCO1_RAT
18	21.6	3564	1 CSM1_MOUSE	
19	184.5	21.4	3565	1 CSM1_HUMAN
20	182	21.1	3487	1 CSM2_HUMAN
21	178.5	20.7	699	1 CRAR_HUMAN
22	173.5	20.1	597	1 RPL10_PARLI
23	163.5	19.0	2796	1 CSM3_MOUSE
24	163.5	19.0	1	1 CSM3_HUMAN
25	162.5	18.9	704	1 CRAR_MOUSE
26	161.5	18.7	859	1 SNT7_HUMAN
27	160.5	18.6	616	1 SPAN_STRPU
28	152.5	17.7	705	1 CIR_HUMAN
29	151	17.5	1	1 TSG6_MOUSE
30	151	17.5	277	1 TSG6_HUMAN
31	150	17.4	310	1 ASTL_COTJA
32	149.5	17.3	855	1 ST14_HUMAN
33	148	17.2	276	1 TSG6_RABIT

ALIGNMENTS

34	142.5	16.5	514	1 UVSS2_XENLA	P42664 xenopus lae
35	136.5	15.8	855	1 ST14_MOUSE	P56777 mus musculu
36	129.5	15.0	1428	1 ATRN_MOUSE	Q9WU60 mus musculu
37	127.5	14.8	1429	1 ATRN_HUMAN	Q75882 homo sapien
38	116	13.2	1034	1 ENTP_MOUSE	P987435 mus musculu
39	116	13.5	1069	1 ENTP_MOUSE	Q8ncwo homo sapien
40	115	13.3	462	1 KRM2_HUMAN	P98072 bos tauricus
41	114	13.2	1035	1 ENTP_BOVIN	P15156 mesocricetus auratus
42	111	12.9	695	1 CASP_MESAU	Q00187 homo sapien
43	110	12.8	686	1 MAS2_HUMAN	P80720 equus caballus
44	107.5	12.5	133	1 ANN_HORSE	P09871 homo sapien
45	107.5	12.5	688	1 CIS_HUMAN	

RESULT 1					
ID	NRPI1_CHICK	STANDARD;	PRT;	914 AA.	
AC	P79755;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Neuropilin-1 precursor (AS protein).				
GN	NRPI1 OR NRP1				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
RA	Fujikawa H.;				
RA	SEQUENCE FROM N.A.				
RA	STRAN=White Leghorn; TISSUE=Embryonic brain; MEDLINE=5324761; PubMed=7601310; Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A., [1]				
RT	"Expression of a cell adhesion molecule, neuropilin, in the developing chick nervous system.";				
RT	Dev. Biol. 170:207-222(1995).				
RL	FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsive activity of semaphorins (By similarity). Seems to have calcium-independent cell adhesion properties.				
CC	-!- TISSUE SPECIFICITY: Developing nervous system; optic tectum (layers D and E of GFS), amacrine cells of retina, neurites of dorsal root ganglia. Also expressed in nonneuronal cells, e.g. blood vessel in the entire embryo.				
CC	-!- SIMILARITY: Belongs to the neuropilin family.				
CC	-!- SIMILARITY: Contains 2 CUB domains.				
CC	-!- SIMILARITY: Contains 1 FN5/8 type C domains.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL; D5416; BAA8256.1; -; HSSP; PI2259; ICZT; InterPro; IPR00850; CUB. InterPro; IPR00421; FAB5_C. InterPro; IPR008979; Galbind like. InterPro; IPR00998; MAM_domain. Pfam; PF00431; CUB; 2. Pfam; PF00754; F5_F8_type_C; 2. Pfam; PF00629; MAM; 1.				

DR MGD; MGI:BB176; Bmp1.

DR InterPro; IPR00152; Asx_hydroxyl_S.

DR InterPro; IPR00085; CUB.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_Like.

DR InterPro; IPR006025; Pept_M_Zn_BS.

DR InterPro; IPR006026; Peptidase_M.

DR InterPro; IPR001506; Peptidase_M12A.

DR Pfam; PF01440; Astacin; 1.

DR Pfam; PF00431; CUB; 5.

DR Pfam; PF00008; EGF; 2.

DR PRINTS; PRO0480; ASFCIN.

DR SMART; SMC0179; EGF_Ca; 2.

DR SMART; SM0035; Zinc; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE; PS00180; CUB; 5.

DR PROSITE; PS00182; EGF; 1; FALSE_NEG.

DR PROSITE; PS00186; EGF; 2.

DR PROSITE; PS00026; EGF; 3; 2.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

KW Hydrolase; Metalloprotease; Repeat; Osteogenesis; Chondrogenesis; Zinc; Growth factor; Cytokine; Zinc; Calcium; Signal; Glycoprotein; Zymogen.

KW SIGNAL; 1

FT SIGNAL; 25

FT PROPE; 25

FT CHAIN; 126

FT DOMAIN; 126

FT DOMAIN; 327

FT DOMAIN; 440

FT DOMAIN; 552

FT DOMAIN; 593

FT DOMAIN; 708

FT DOMAIN; 752

FT DOMAIN; 864

FT DOMAIN; 865

FT METAL; 218

FT ACT_SITE; 219

FT METAL; 222

FT METAL; 228

FT DISULFID; 188

FT DISULFID; 327

FT DISULFID; 380

FT DISULFID; 440

FT DISULFID; 493

FT DISULFID; 556

FT DISULFID; 564

FT DISULFID; 577

FT DISULFID; 579

FT DISULFID; 596

FT DISULFID; 649

FT DISULFID; 712

FT DISULFID; 719

FT DISULFID; 734

FT CARBOHYD; 96

FT CARBOHYD; 147

FT CARBOHYD; 337

FT CARBOHYD; 368

FT CARBOHYD; 604

SEQUENCE; 991 AA; 111607 MW; 68A1847783A0B99E CRC64;

Query Match 26.0%; Score 224; DB 1; Length 991; Best Local Similarity 33.6%; Pred. No. 3 3e-15; Matches 43; Conservative 27; Mismatches 16; Indels 16; Gaps 2;

Qy 26 GRBKQTSSETQSVQCGTWTKAEGGIFTSPNYPSPKPPDRSIVIIRAPQCIELYFD 85

Qy 751 GRBKQTSSETQSVQCGTWTKAEGGIFTSPNYPSPKPPDRSIVIIRAPQCIELYFD 795

Qy 86 EKYSIESPWECKEDHIEVRDGPFGFSPPTIGRTECGQONPVPVIGSGRFLWIKFADGELES 145

Db 796 E-MDIESOPECAVDHLEVFDFGDKAKAPVILGRFCGSKKEPVPVATGNMFLRFLYSDNSVQR 854

Db Qy

Db 855 KGFOASHS 862

Db

RESULT 7

NRP1_HUMAN

ID NRP1_HUMAN STANDARD; PRT; 923 AA.

AC 014786; 060461; (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor)

DR NRP1_OR_NRP_OR_VEGF165R.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OC NCBI_TaxID=9606;

RN [1] NRP1_HUMAN STANDARD; PRT; 923 AA.

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=9743304; PubMed=9288753;

RA He Z., Tessier-Lavigne M.; "Neuropilin is a receptor for the axonal chemorepellent semaphorin III.", Cell 90:739-751(1997).

RL RN [2] NRP1_HUMAN STANDARD; PRT; 923 AA.

RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.

RC TISSUE=Breast;

RX MEDLINE=9918809; PubMed=9529350;

RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.", Cell 92:735-745(1998).

RN [3] NRP1_HUMAN STANDARD; PRT; 923 AA.

RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.

RC TISSUE=Prostatic adenocarcinoma;

RX MEDLINE=20183929; PubMed=10688880;

RA Gagnon M.L., Bieenberg D.R., Gechman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.; "Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity.", Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578 (2000).

RL RN [4] NRP1_HUMAN STANDARD; PRT; 923 AA.

RP CHARACTERIZATION;

RX MEDLINE=20309748; PubMed=10748121;

RA Gluzman-Poltorak Z., Cohen T., Herzig Y., Neufeld G.; "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor 2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";

RL J. Biol. Chem. 275:18404-18405(2000).

CC -!- FUNCTION: The membrane-bound isoform 1 is a receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsive activity of semaphorins. It binds to Sema3A, The PLGF-2 isoform of PGP, The VEGF-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis. It may regulate VEGF-induced angiogenesis

CC -!- FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to inhibit its binding to cells. It may also induce apoptosis by sequestering VEGF-165. May bind as well various members of the semaphorin family. Its expression has an adverse effect on blood vessel number and integrity.

CC -!- SUBCELLULAR_LOCATION: Type I membrane protein. Isoform 2 is secreted.

CC -!- ALTERNATIVE_PRODUCTS:

CC Event=Alternative_splicing; Named isoforms=2;

CC Name=1; Synonyms=Membrane-bound;

CC Name=2; Synonyms=Soluble; Sequence=Displayed;

FT	VARSPPLIC	824	986	/FTId=VSP_005469. Missing in isoform EMP1-7.
FT	PT			/FTId=VSP_005470.
FT	CONFLICT	748	748	D -> N (IN REF. 4).
FT	CONFFLICT	934	934	R -> S (IN REF. 4).
SQ	SEQUENCE	986 AA;	111248 MW;	F83201913AC3GBEA CRC64;
Qy				Query Match 25.6%; Score 220.5; DB 1; Length 986;
				Best Local Similarity 38.2%; Pred. No. 7.6e-15; Mismatches 38; Indels 1; Gaps 1;
				Matches 39; Conservative 24; Misnatches 38; Indels 1; Gaps 1;
Db				51 SPIGRPCGQONPPVKSSKETTAISSTPGRVKTLEM-GMDIESQPCAYDILEVFDGDRAK 814
Qy		111		511 SPIGRPCGQONPPVKSSKETTAISSTPGRVKTLEM-GMDIESQPCAYDILEVFDGDRAK 814
Db		815		815 APVLGSPCGSKRPEPVULATSGRMFLRFYPSNSVQKGFQASH 856
RESULT	9			
TLD_BRARE				
ID	TLD_BRARE			STANDARD;
AC	0574460;			PRT; 1022 AA.
DT	16-OCT-2001			(Rel. 40, Created)
DT	16-OCT-2001			(Rel. 40, Last sequence update)
DE	Dorsal-ventral patterning tollloid protein precursor			(EC 3.4.24.-)
DE	(Mini fin protein)			
GN	Tolloid or TLD or MFN.			
OS	Brachydanio rerio (Zebrafish)			(Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX				
RN	111			[1]
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
RC	TISSUE=Gastrula;			
RX	MEDLINE=9805457; PubMed=9395394;			
RA	Blader P., Rastegar S., Fischer N., Strähle U.;			
RA	"Cleavage of the BMP-4 antagonist chordin by zebrafish Tollloid".			
RT	Science 278:1937-1940(1997).			
RL				[2]
RN				
RP	FUNCTION, AND TISSUE SPECIFICITY.			
RX	MEDLINE=993076; PubMed=10375503;			
RA	Connors S.A., Trout J., Bakker M., Mullins M.C.;			
RT	"The role of tollloid/mini fin in dorsoventral pattern formation of the zebrafish embryo."			
RT	Development 126:3119-3130(1999).			
RL				
CC	-!- FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic protein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP from inactive complexes.			
CC	-!- TISSUE SPECIFICITY: During gastrulation, accumulates around the development of the tail.			
CC	-!- TISSUE SPECIFICITY: During gastrulation, accumulates around the closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-somite stage, expressed in the developing tail bud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoietic system.			
CC	-!- SIMILARITY: Belongs to peptidase family M12A.			
CC	-!- SIMILARITY: Contains 2 EGF-like domains.			
CC	-!- SIMILARITY: Contains 5 CUB domains.			
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DR	EMBL; AF027596; AAC60304.1; -;			
DR	RRSP; P35555; 1E9N.			
DR				
DR	MEROPS; M12_016; -;			
ZFIN	ZDB-GENE-990415-265; tolloid.			
DR	InterPro; IPR00152; Asx-hydroxyl_S.			
DR	InterPro; IPR00859; CUB.			
DR	InterPro; IPR0181; EGF_Ca.			
DR	InterPro; IPR06209; EGF_Like.			
DR	InterPro; IPR06025; Pept_M_Zn_BS.			
DR	InterPro; IPR06026; Peptidase_M.			
DR	InterPro; IPR01506; Peptidase_M12A.			
DR	Pfam; PF00431; Astacin; 1.			
DR	Pfam; PF0008; EGF; 2.			
DR	PRINTS; PR00487; CUB; 5.			
DR	SMART; SM00179; EGF_Ca; 2.			
DR	SMART; SM0035; Zinc; 1.			
DR	PROSITE; PS0010; ASX_HYDROXYL; 2.			
DR	PROSITE; PS00180; Zinc_Ca; 2.			
DR	PROSITE; PS00142; EGF_1; 2.			
DR	PROSITE; PS50026; EGF_3; 2.			
DR	PROSITE; PS001187; EGF_2.			
DR	PROSITE; PS00142; Zinc_Protease; 1.			
DR	Devellopmental protein; Hydrolase; Protease; Metalloprotease; Zinc;			
KW	Mettal-binding; Calcium; EGF-like domain; Repeat; Signal; Glycoprotein;			
KW	Zymogen.			
FT	SIGNAL	1	32	POTENTIAL.
FT	PROPEP	33	156	DORSAL-VENTRAL PATTERNING TOLLOID
FT	CHAIN	157	1022	PROTEIN.
FT	DOMAIN	157	357	METALLOPROTEASE (BY SIMILARITY).
FT	DOMAIN	358	470	CUB 1.
FT	DOMAIN	471	583	CUB 2.
FT	DOMAIN	583	624	EGF-LIKE 1; CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	627	739	CUB 3.
FT	DOMAIN	739	779	EGF-LIKE 2; CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	783	895	CUB 4.
FT	DOMAIN	896	1012	CUB 5.
FT	METAL	249	249	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT-SITE	250	250	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	253	253	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	259	259	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	358	384	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	411	433	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	471	497	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	524	546	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	587	599	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	595	608	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	610	623	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	627	653	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	680	702	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	743	754	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	750	763	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	765	778	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	783	809	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	836	858	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	896	925	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISUFDID	953	975	ZINC (CATALYTIC) (BY SIMILARITY).
FT	CARBHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	368	368	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	399	399	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	635	635	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1022 AA;	115536 MW;	A68CALD084179-F9 CRC64;
Qy				Query Match 25.6%; Score 220.5; DB 1; Length 1022;
				Best Local Similarity 40.4%; Pred. No. 7.9e-15; Mismatches 42; Indels 1; Gaps 1;
				Matches 42; Conservative 19; Misnatches 42; Indels 1; Gaps 1;

FT	DISULFID	330	380	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 2 F5/8 type C domains.
FT	DISULFID	407	429	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 1 MAM domain.
FT	DISULFID	468	495	BY SIMILARITY.	CC	-----
FT	DISULFID	522	544	BY SIMILARITY.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	DISULFID	585	596	BY SIMILARITY.	CC	between the European Bioinformatics Institute. There are no restrictions on its
FT	DISULFID	592	605	BY SIMILARITY.	CC	use by non-profit institutions as long as its content is in no way
FT	DISULFID	607	620	BY SIMILARITY.	CC	modified and this statement is not removed. Usage by and for commercial
FT	DISULFID	624	652	BY SIMILARITY.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
FT	DISULFID	683	706	BY SIMILARITY.	CC	or send an email to license@isb-sib.ch).
FT	DISULFID	747	759	BY SIMILARITY.	CC	-----
FT	DISULFID	754	767	BY SIMILARITY.	CC	
FT	DISULFID	769	782	BY SIMILARITY.	DR	DR EMBL; AF016296; AAC33371; -.
FT	DISULFID	787	813	BY SIMILARITY.	DR	HSSP; P12259; ICZT.
FT	DISULFID	840	862	BY SIMILARITY.	DR	InterPro; IPR00859; CUB.
FT	DISULFID	900	930	BY SIMILARITY.	DR	InterPro; IPR00421; F58C.
FT	DISULFID	957	979	BY SIMILARITY.	DR	InterPro; IPR008979; Gal bind like.
FT	CARBHYD	166	166	BY SIMILARITY.	DR	InterPro; IPR00998; MAM_domain.
FT	CARBHYD	431	431	BY SIMILARITY.	DR	Pfam; PF00754; F5_8_type_C; 2.
FT	CARBHYD	533	533	BY SIMILARITY.	DR	Pfam; PF00622; MAM_1.
FT	CARBHYD	634	634	BY SIMILARITY.	DR	PRINTS; PR00024; MAMODATN.
FT	CARBHYD	667	667	BY SIMILARITY.	DR	SMART; SM0042; CUB; 2.
FT	CARBHYD	781	781	BY SIMILARITY.	DR	SMART; SM00231; FAS8C; 2.
FT	CARBHYD	854	854	BY SIMILARITY.	DR	SMART; SM00137; MAM; 1.
FT	CARBHYD	908	908	BY SIMILARITY.	DR	PROSITE; PS01180; CUB; 2.
FT	SEQUENCE	120575	MM; 76F4B3AB7996FBA CRC64;	-----	DR	PROSITE; PS01285; FAS8C_1; 2.
QY	39	VQCGGWTWKAEGGIFTSPNPKSPSKYPPRECIVYIIEA-APROCYIELFDEKSI-IEPKSWECKR 98	-----	DR	PROSITE; PS01286; FAS8C_2; 2.	
QY	466	VVCGGGDLKLTKDOSIDSPNPKSPNPKSPSKYPPRECIVYIIEA-APROCYIELFDEKSI-IEPKSWECKR 524	-----	DR	PROSITE; PS50022; FAS8C_3; 2.	
QY	99	DHIEFRDGGPRGFSPPIGFRGQQNPPVIKSSEGRFLWIKFEPADGELESMGSSA 150	-----	DR	PROSITE; PS00740; MAM_1; 1.	
QY	525	DFEVRDGGNDSRIGFRGFGDKEPLPNIKRSQMNIFRVSDDSSVQKGSSA 576	-----	DR	PROSITE; PS50060; MAM_2; 1.	
RESULT 11	NRPL_RAT	STANDARD;	PRT;	922 AA.	KW	Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
ID	NRPL_RAT				FT	SIGNAL
AC	Q90WJ9;				FT	1
DT	16-OCT-2001	(Rel. 40, Created)			FT	21
DT	16-OCT-2001	(Rel. 40, last sequence update)			FT	POTENTIAL.
DT	28-FEB-2003	(Rel. 41, Last annotation update)			FT	NEUROPILIN-1.
DE	Neuropilin-1 precursor (vascular endothelial cell growth factor 165 receptor).				FT	EXTRACELLULAR (POTENTIAL).
DB					FT	F5/8 TYPE C 1.
GN	NRPL.				FT	CYTOSLAMIC (POTENTIAL).
OS	Rattus norvegicus (Rat).				FT	CUB 1.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				FT	F5/8 TYPE C 2.
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.				FT	MAM.
OX	NCBI_TaxID=10116;				FT	PROBABLE.
RN	[1]				FT	PROBABLE.
RP	SEQUENCE FROM N.A.				FT	PROBABLE.
RC	STRAIN-Sprague-Dawley;				FT	PROBABLE.
RX	MEDLINE:97433085; PubMed=9288754;				FT	PROBABLE.
RA	Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,				FT	PROBABLE.
RA	Ginty D.D.;				FT	PROBABLE.
RL	"Neuropilin is a semaphorin III receptor.";				FT	BY SIMILARITY.
RL	Cell 90: 753-762(1997).				FT	BY SIMILARITY.
CC	It may regulate VEGF-induced angiogenesis (By similarity).				FT	BY SIMILARITY.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				FT	BY SIMILARITY.
CC	-!- TISSUE SPECIFICITY: Found in the embryonic nervous system.				FT	BY SIMILARITY.
CC	-!- SIMILARITY: Belongs to the neuropilin family.				FT	BY SIMILARITY.
CC	increased VEGF-165 binding to KDR as well as increased chemotaxis.				FT	BY SIMILARITY.
RESULT 12	NRPL_MOUSE	STANDARD;	PRT;	923 AA.	QY	37 KSVQCGGWTWKAEGGIFTSPNPKSPSKYPPRECIVYIIEA-APROCYIELFDEKSI-IEPKSWECKR 95
ID	NRPL_MOUSE				Db	23 RSKQKGCTIKTENPGYLTSPGYPSYHSEKCBWLQAPPKRIMNPNPHEDLEDR-D 81
AC	P97333;				QY	96 CKFDEHTRDGGPRGFSPPIGFRGQQNPPVIKSSEGRFLWIKFEPADGELESMGSSA 152
DT	01-NOV-1997 (Rel. 35, Created)				Db	82 CKDIDYEVIDGENEGGRIGWKGFKCRAKAPSPVSSGPFFIKFVSDYETHGAGSIRY 138

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CC

DR EMBL: L37799; AA61949.1; ALT_SEQ.

DR EMBL: AB08545; AAU23281.1; -.

DR EMBL: AF053356; AAC18800.1; -.

DR EMBL: AF083655; AAD16041.1; -.

DR EMBL: BC000574; AAH00574.1; -.

DR EMBL: BC032205; AAH32205.1; -.

DR Genew HGNC:8738; PCOLCE.

DR MIM: 600270; -.

DR GO: GO:0008151; P:cell growth and/or maintenance; TAS.

DR GO: GO:0007275; P:development; TAS.

DR Interpro; IPR00134; Netrin_C.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF01759; NTR; 1.

DR SMART; SM00643; C345C; 1.

DR SMART; SM00042; CUB; 2.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS05189; NTR; 1.

KW Glycoprotein; Repeat; Signal.

FT SIGNAL 1

FT CHAIN 26

FT PROCOLLAGEN 449

FT C-PROTEINASE 449

FT ENHANCER PROTEIN.

FT DOMAIN 37

FT CUB 1.

FT DOMAIN 159

FT CUB 2.

FT DOMAIN 318

FT NTR 437

FT CLEAVAGE.

FT SITE 287

FT CLEAVAGE.

FT SITE 288

FT CLEAVAGE.

FT SITE 293

FT CLEAVAGE.

FT SITE 299

FT CLEAVAGE.

FT SITE 303

FT CLEAVAGE.

FT CARBOHYD 29

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 431

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 449 AA; 47972 MW; 3D88430150648796 CRC64;

Query Match 23.4%; Score 201.5; DB 1; Length 449; Best Local Similarity 37.1%; Pred. No. 2; e=13; Matches 53; Conservative 20; Mismatches 57; Indels 13; Gaps 5;

QY 16 IHLISGATKKGKIKQKOTSETQSVQCGWTKHAEGGIFTSPWYF-SKXPPRECIVIEA 74

Db 143 LAMYSGRATSGTQHQF-----CGGRLEAQGTL-TTPNWPESDYPPGICSWHIA 192

QY 75 APROCIETYFDKYSIERSWECKFDHIEVDRDGPFG-FSPIIIFRCGQONPPVKKSSRFL 133

Db 193 PPOVIAILTF-EKFDLDTYCRYDSV/SVNGAVSDSRRIKFCGDAVPGSISSEGNEI 251

QY 134 WIKPFADEBLMSGFSARYNFTP 156

Db 252 LWQFVSDLSVTADGFSASVYKTLP 274

RESULT 15

NPBP1_XENLA STANDARD; PRT; 928 AA.

AC P28824;

DT 01-DEC-1992 (Rel. 24, Created)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DR Neuropilin-1 precursor (A5 protein) (A5 antigen).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodidae; Xenopus.

OC NCBITaxID:8355;

RN [1]

RP SOURCE FROM N.A.

RC TISSUE:Brain;

RA MEDLINE=91337458; PubMed=1908252;

RA Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;

RT "The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";

RT Neuron 7:295-307 (1991).

RL -

CC -

CC FUNCTION: Receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorrepulsive activity of semaphorins (By similarity). Presumed to be involved in the neuronal recognition between the optic nerve fibers and the visual centers.

CC -

CC SUBCELLULAR LOCATION: Type I membrane protein.

CC -

CC TISSUE SPECIFICITY: Retinal ganglion cells and visual center neurons.

CC -

CC SIMILARITY: Belongs to the neuropilin family.

CC -

CC SIMILARITY: Contains 2 CUB type C domains.

CC -

CC SIMILARITY: Contains 1 MAM domain.

CC -

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CC -

CC EMBL: D10467; BAM01260.1; -.

DR HSSP; P12259; IC27.

DR Interpro; IPR000859; CUB.

DR Interpro; IPR00421; FAS8_C.

DR Interpro; IPR00579; Gal Bind like.

DR Interpro; IPR000998; MAM_domain.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00754; F5_F8_type_C; 2.

DR Pfam; PF00529; MAM; 1.

DR PRINTS; PR00020; MAM DOMAIN.

DR SMART; SM00231; CUB; 2.

DR SMART; SM00137; MAM; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; FAS8_C; 2.

DR PROSITE; PS01286; FAS8_C-2; 2.

DR PROSITE; PS05022; FAS8_C-3; 2.

DR PROSITE; PS00740; MAM; 1.

DR PROSITE; PS50067; MAM-2; 1.

DR PROSITE; PS50068; MAM-3; 1.

DR PROSITE; PS50069; MAM-4; 1.

DR PROSITE; PS50070; MAM-5; 1.

DR PROSITE; PS50071; MAM-6; 1.

DR PROSITE; PS50072; MAM-7; 1.

DR PROSITE; PS50073; MAM-8; 1.

DR PROSITE; PS50074; MAM-9; 1.

DR PROSITE; PS50075; MAM-10; 1.

DR PROSITE; PS50076; MAM-11; 1.

DR PROSITE; PS50077; MAM-12; 1.

DR PROSITE; PS50078; MAM-13; 1.

DR PROSITE; PS50079; MAM-14; 1.

DR PROSITE; PS50080; MAM-15; 1.

DR PROSITE; PS50081; MAM-16; 1.

DR PROSITE; PS50082; MAM-17; 1.

DR PROSITE; PS50083; MAM-18; 1.

DR PROSITE; PS50084; MAM-19; 1.

DR PROSITE; PS50085; MAM-20; 1.

DR PROSITE; PS50086; MAM-21; 1.

DR PROSITE; PS50087; MAM-22; 1.

DR PROSITE; PS50088; MAM-23; 1.

DR PROSITE; PS50089; MAM-24; 1.

DR PROSITE; PS50090; MAM-25; 1.

DR PROSITE; PS50091; MAM-26; 1.

DR PROSITE; PS50092; MAM-27; 1.

DR PROSITE; PS50093; MAM-28; 1.

DR PROSITE; PS50094; MAM-29; 1.

DR PROSITE; PS50095; MAM-30; 1.

DR PROSITE; PS50096; MAM-31; 1.

DR PROSITE; PS50097; MAM-32; 1.

DR PROSITE; PS50098; MAM-33; 1.

DR PROSITE; PS50099; MAM-34; 1.

DR PROSITE; PS50100; MAM-35; 1.

DR PROSITE; PS50101; MAM-36; 1.

DR PROSITE; PS50102; MAM-37; 1.

DR PROSITE; PS50103; MAM-38; 1.

DR PROSITE; PS50104; MAM-39; 1.

DR PROSITE; PS50105; MAM-40; 1.

DR PROSITE; PS50106; MAM-41; 1.

DR PROSITE; PS50107; MAM-42; 1.

DR PROSITE; PS50108; MAM-43; 1.

DR PROSITE; PS50109; MAM-44; 1.

DR PROSITE; PS50110; MAM-45; 1.

DR PROSITE; PS50111; MAM-46; 1.

DR PROSITE; PS50112; MAM-47; 1.

DR PROSITE; PS50113; MAM-48; 1.

DR PROSITE; PS50114; MAM-49; 1.

DR PROSITE; PS50115; MAM-50; 1.

DR PROSITE; PS50116; MAM-51; 1.

DR PROSITE; PS50117; MAM-52; 1.

DR PROSITE; PS50118; MAM-53; 1.

DR PROSITE; PS50119; MAM-54; 1.

DR PROSITE; PS50120; MAM-55; 1.

DR PROSITE; PS50121; MAM-56; 1.

DR PROSITE; PS50122; MAM-57; 1.

DR PROSITE; PS50123; MAM-58; 1.

DR PROSITE; PS50124; MAM-59; 1.

DR PROSITE; PS50125; MAM-60; 1.

DR PROSITE; PS50126; MAM-61; 1.

DR PROSITE; PS50127; MAM-62; 1.

DR PROSITE; PS50128; MAM-63; 1.

DR PROSITE; PS50129; MAM-64; 1.

DR PROSITE; PS50130; MAM-65; 1.

DR PROSITE; PS50131; MAM-66; 1.

DR PROSITE; PS50132; MAM-67; 1.

DR PROSITE; PS50133; MAM-68; 1.

DR PROSITE; PS50134; MAM-69; 1.

DR PROSITE; PS50135; MAM-70; 1.

DR PROSITE; PS50136; MAM-71; 1.

DR PROSITE; PS50137; MAM-72; 1.

DR PROSITE; PS50138; MAM-73; 1.

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Job time : 18 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 18:21:16 ; Search time 21 seconds

(without alignments)
723.727 Million cell updates/sec

Title: US-09-887-593A-2
Perfect score: 862
Sequence: 1 MIHGSQLVHLIVASLTLIHLSD...ADGELESMSGFSARYNFTPGK 158
Scoring table: BioSUM52
Gapop 10.0 , Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: pir1:*

2:

pir2:*

3:

pir3:*

4:

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Length	DB ID	Description
1	818	94.9	533	2 JCT985	brain-specific CUB hypothetical prote
2	260	30.2	321	1 T33161	intrinsic factor-B intrinsic factor-B
3	227.5	26.4	3623	2 T08618	procollagen C-endo
4	227.5	26.4	3623	2 T04546	procollagen C-endo
5	227	26.3	3702	1 JCT985	procollagen C-endo
6	224	26.0	991	2 T49540	hypothetical prote
7	220.5	25.6	986	1 B57788	intrinsic factor-B
8	217.5	25.2	1057	1 A39288	procollagen C-endo
9	216.5	25.1	1464	2 S55984	dorsal-ventral pat
10	211	24.5	730	1 BM701	development Protei
11	211	24.5	823	1 A53788	procollagen C-endo
12	199.5	23.1	1070	2 T31069	procollagen C-endo
13	199	23.1	579	2 JCT629	tollloid-BMP-1 like
14	198.5	23.0	927	1 J00948	membrane-type friz
15	197.5	22.9	449	2 A55362	A5 antigen precurs
16	193.5	22.4	402	2 JH0403	procollagen I C-pr
17	187.5	21.8	1594	2 T30549	procollagen I C-pr
18	178.5	20.7	699	1 I54763	hensin - rabbit
19	172.5	20.0	2403	2 A59386	Ra-reactive factor
20	172.5	19.9	174	2 T33161	sanko - human
21	170.5	19.8	597	2 S71352	polyprotein - Afri
22	164.5	19.1	2083	2 T27271	metalloproteins
23	162.5	18.9	504	2 S56745	CRP-ductin-alpha p
24	161.5	18.7	3871	2 T22812	mucin (clone P031)
25	152.5	17.7	705	1 C1HURB	hypothetical prote
26	151	17.5	275	2 JG6506	complement subcomp
27	151	17.5	277	2 A41735	tumor necrosis fac
28	150	17.4	310	2 S41055	hyaluronate-bindin
29	149	17.3	1290	2 A57190	metalloprotease
					ebnezin precursor

ALIGNMENTS

30	148	17.2	276	2 A47290	TSG-6 homolog PS4
31	146	16.9	412	2 S72579	hypothetical prote
32	145	16.8	421	2 T25393	hypothetical prote
33	143.5	16.6	288	2 T33224	hypothetical prote
34	143.5	16.6	417	2 T20159	hypothetical prote
35	142.5	16.5	319	2 15169	UWS-2 protein - Af
36	142.5	16.5	767	2 T30018	hypothetical prote
37	141.5	16.4	855	2 JC7732	membrane-bound arg
38	137	15.9	1004	2 T30338	ovoiductin (EC 3.4)
39	131	15.2	416	2 T2048	hypothetical prote
40	128	14.8	383	2 T21946	LDL receptor relat
41	125	14.5	770	2 T00203	spinal cord-derive
42	123	14.3	770	2 T00204	hypothetical prote
43	122.5	14.2	370	2 JC7592	spinal cord-derive
44	121	14.1	417	2 T29854	hypothetical prote
45	118	13.7	370	2 JC7591	spinal cord-derive

RESULT 1
JCT985
brain-specific CUB and LDLa domain-containing transmembrane protein, BTCL1 protein - M
C.Species: *Mus musculus* (house mouse)
C.Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C.Accession: JC7985; PC7228
R.Michishita, M.; Ikeda, T.; Nakashiba, T.; Osawa, M.; Tashiro, K.; Honjo, T.; Doi, K.
Biochem. Biophys. Res. Commun. 306, 680-686, 2003
A.Title: A novel gene, Btcl1, encoding a CUB and LDLa domains is expressed in restricted
A.Reference number: JC7985; PMID:12810072
A.Accession: JC7985
A.Molecule type: mRNA
A.Residues: 1-533 <MIC>
A.Cross-references: GB:AM138990
A.Experimental source: Cerebellum, 3-week-old
A.Molecule type: protein
A.Genetics:
C;Keywords: BTCL1 protein; CUB domain; LDLa domain; transmembrane protein.

Query Match 94.9%; Score 818; DB 2; Length 533;
Best Local Similarity 94.2%; Pred. No. 6.1e-76;
Matches 147; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 2
T33161
hypothetical protein K03E5.1 - *Caenorhabditis elegans*
C.Species: *Caenorhabditis elegans*
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T33161
R.Becker, M.; Graves, T.; Fronick, B.
submitted to the EMBL Data Library, May 1998
A.Description: The sequence of C. elegans cosmid K03E5.
A.Reference number: 221294
A;Accession: T33161

A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-321 <B3C>
 A;Cross-references: EMBL:AF034611; NID:9329528; PIDN: AAC82612.1; PID:9329529
 C;Genetics:
 A;Map position: 10p12
 C;Keywords: receptor; vitamin B12 uptake
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-3623/Domain: intrinsic factor-B12 receptor #status predicted <MAT>
 F;436-467/Domain: EGF homology <EGF>

Query Match 30.2%; Score 260; DB 2; Length 321;
 Best Local Similarity 43.5%; Pred. No. 6; 3e-19; Indels 8; Gaps 2;
 Matches 50; Conservative 20; Mismatches 37; Indels 8; Gaps 2;
 Best Local Similarity 43.5%; Pred. No. 6; 3e-19; Indels 8; Gaps 2;
 Matches 50; Conservative 20; Mismatches 37; Indels 8; Gaps 2;

QY 52 IFTSPNPKSPYKPPRECIVTEAAPRCIELYDEKYSIESPSW-----ECKFDHIEVR 104
 DB 75 IFTSPNPKSPYKPPRECIVTEAAPRCIELYDEKYSIESPSW-----ECKFDHIEVR 134

QY 105 DGPFGFSPITIGRFGCGQQNPP-WTKSSGRFLWIKFFADGELESMGFSARYNFTPGK 158
 DB 135 DGRYGFSPLIARFCGDRVPKREIRAVSGFLWIKRFRSDMSMLEYQGFSAYATVPSK 189

RESULT 3
 T08618 intrinsic factor-B12 receptor CUBILIN precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
 C;Accession: T08618
 R;Moestrup, S.K.; Kozzak, R.; Kristiansen, M.; Karsen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
 A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
 A;Reference number: 216459; MUID:98148073; PMID:9478979
 A;Accession: T08618
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Cross-references: EMBL:AF022247; NID:93834379; PIDN: AAC71661.1; PID:93834380
 C;Genetics:
 A;Gene: CUBILIN
 C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology <EGF>
 C;Keywords: egg-yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
 C;KeyWords: signal sequence #status predicted <SIG> #status predicted <MAT>
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-3623/Domain: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
 F;33-184/Domain: EGF homology <EGF>
 F;436-467/Domain: EGF homology <EGF>

Query Match 26.4%; Score 227.5; DB 2; Length 3623;
 Best Local Similarity 37.5%; Pred. No. 2.1e-14; Indels 45; Gaps 2;
 Matches 45; Conservative 26; Mismatches 46; Indels 3; Gaps 2;

QY 37 RSVOCG-TWTHKABG-GIFTSPNPKSPYKPPRECIVTEAAPRCIELYDEKYSIESPSW-----ECKFDHIEVR 93
 DB 2213 RSVOCG-TWTHKABG-GIFTSPNPKSPYKPPRECIVTEAAPRCIELYDEKYSIESPSW-----ECKFDHIEVR 2272

QY 94 WECKFDHIEVRDGPFGFSPITIGRFGCGQQNPPVTKSSGRFLWIKFFADGELESMGFSARYNFTPGK 153
 DB 2273 PNCTSPNPKYHLRDEGVDTSAPLISKPGTSLPSSQWSSGQVWMLRPSDNPSPTHVGKAKYS 2332

QY 154 F-----FTPGK 158
 DB 2333 IAQCGGRVFGQ 2343

RESULT 5
 JC2218 procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
 N;Alternate name: bone morphogenic protein 1
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
 C;Accession: JC2218
 R;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H. Gene 134, 257-261, 1993
 A;Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein
 A;Reference number: JC2218; MUID:94085787; PMID:8262384
 A;Accession: JC2218
 A;Molecule type: mRNA
 A;Residues: 1-707 <MAE>
 A;Cross-references: GB:112249; NID:9406540; PIDN: AAC16313.1; PID:9406541
 C;Comment: This protein induces ectopic cartilage formation in vivo.
 C;Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology;
 C;Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
 F;93-284/Domain: astacin homology <AST>
 F;205-397/Region: complement 1r/s-like repeat
 F;205-394/Domain: Cir/Cis repeat homology <C1R1>
 F;398-507/Region: complement 1r/s-like repeat
 F;398-507/Domain: Cir/Cis repeat homology <C1R2>
 F;514-550/Domain: EGF homology <EGF>
 F;554-663/Region: complement 1r/s-like repeat
 F;554-663/Domain: Cir/Cis repeat homology <C1R3>
 F;62-105, 295-326/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;177/Active site: Glu #status predicted
 F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 26.3%; Score 227; DB 2; Length 707;
 Best Local Similarity 40.2%; Pred. No. 3.7e-15; Indels 45; Gaps 2;
 Matches 45; Conservative 18; Mismatches 47; Indels 2; Gaps 2;

QY 41 CGTWTKHEAGGIFTSPNPKSPYKPPRECIVTEAAPRCIELYDEKYSIESPSWCKFDH 100
 DB 398 CGGEVKKDSGHT-QSNPYPDPRPKACWKLVSSEGFHVGISF-QSFELERHDSCAYD 455

QY 101 IFRDGPFGFSPITIGRFGCGQQNPPVTKSSGRFLWIKFFADGELESMGFSARY 152
 DB 456 IFRDGSSETSPIVGRCPGYDKPDDIKSNTQIWIKEVSDGSINKAGFSINY 507

RESULT 6
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Accession: T09456; MUID:98241400; PMID:9572993
 A;Status: preliminary; translated from GB/EMBL/DBJ

I49540
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
 Dev. Biol. 163, 175-183, 1994
 A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
 A;Reference number: I49540; MUID:94229342; PMID:8174772
 A;Accession: I49540
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residues: 1-991 <RES>
 A;Cross-references: GB:L24755; NID:9439606; PIDN:AAA37306.1; PID:9439607
 C;Genetics:
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
 C;Keywords: hydrolase; metalloproteinase; zinc
 F;135-326-/Domain: astacin homology <AST>
 F;556-592-/Domain: EGF homology <EG1>
 F;595-705-/Domain: C1r/C1s repeat homology <C1R>
 F;712-747-/Domain: EGF homology <EG2>
 F;218-228, 277-/Binding site: zinc (His, His, His, His, Tyr) #status predicted
 F;219-/Active site: Glu #status predicted

Query Match 26.0%; Score 224; DB 2; Length 991;
 Best Local Similarity 33.6%; Pred. No. 1 1e-14; Mismatches 42; Indels 16; Gaps 2;
 Matches 43; Conservative 27; Mismatches 42; Indels 16; Gaps 2;

Qy 26 GPKQQTSETQKVQCGTTWKAEGGFTSPNPKVPPDRCIYIIEAAPQQCIELYF 85
 • Db 751 GCEHKVKTSS-----GTTSPNPKVPPDCKTWAISSTPCHRVKLT 795

Qy 86 EKVISIEFWCKRDHIEVRDGFPGFSPILLGRCQGQNPPIVKSSGRFLWIKFADGELES 145
 • Db 796 E-MDIEQPECAYDHLVEFGRDKAPAVULGRGCGSKKEPEPVLAQNMFLRIVYSDNSVQ 854

Qy 146 MGFSAEYN 153
 • Db 855 KGFQASHS 862

RESULT 7
 B58788
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
 N;Alternate names: bone morphogenic protein 1, tolloid-like splice form
 C;Species: Homo sapiens (man)
 C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
 C;Accession: A37278; B58788
 R;Wozney, J. M.; Rosen, V.; Celeste, A. J.; Mitsock, L. M.; Whitters, M. J.; Kriz, R. W.; Hew
 Science 242, 1528-1534, 1988
 A;Title: Novel regulators of bone formation: molecular clones and activities.
 A;Reference number: A37278; MUID:89072730; PMID:3201241
 A;Accession: A37278
 A;Molecule type: mRNA
 A;Residues: 1-707, 'ERKPAQPPGRGRHQLKERVQKRNTPQ' <W02>
 A;Cross-references: GB:M22488; NID:917949; PIDN:AAA51033.1; PID:9179500
 R;Takahara, K.; Lyons, G.E.; Greenstein, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded
 A;Reference number: A58788; MUID:95096114; PMID:7798260
 A;Accession: B58788
 A;Molecule type: mRNA
 A;Residues 703-96 <TAK>
 A;Cross-references: GB:L35279; NID:9619860; PIDN:AAC41710.1; PID:9619861
 C;Genetics:
 A;Gene: GDB:BMPI; BMP-1
 A;Cross-references: GDB:125203; OMIM:112264
 C;Function:
 A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
 C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g

F;1-22-/Domain: signal sequence #status predicted <SIG>
 F;23-98-/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted
 F;130-321-/Domain: astacin homology <AST>
 F;322-431-/Domain: C1r/C1s repeat homology <C1R>
 F;435-541-/Domain: C1r/C1s repeat homology <C1R>
 F;551-587-/Domain: EGF homology <EG1>
 F;591-700-/Domain: C1r/C1s repeat homology <C1R3>
 F;707-742-/Domain: EGF homology <EG2>
 F;747-856-/Domain: C1r/C1s repeat homology <C1R4>
 F;860-973-/Domain: C1r/C1s repeat homology <C1R5>
 F;91-142,332,363,599-/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;163-319,185-205,322-348,375-397,435-461,488-510,551-553,555-572,574-587,591-617,644-6
 F;213,217,223,272-/Binding site: zinc (His, His, His, His, Tyr) #status predicted
 F;565,720-/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 25.6%; Score 220.5; DB 1; Length 986;
 Best Local Similarity 38.2%; Pred. No. 2.5e-14; Mismatches 38; Indels 1; Gaps 1;
 Matches 39; Conservative 24; Mismatches 38; Indels 1; Gaps 1;

Qy 51 GIFTSPNPKVPPDRCIYIIEAAPQQCIELYFDEKYSIESTPSSWCKDHIFURDGFPGF 110
 • Db 756 GRTTSPWPKPSKSTWAISSTPCHRVKLTME-MDIEQPECAYDHLVEFGRDAK 814

Qy 111 SPITRERFGQKQPVKSGSRFLWIKFADGELES 152
 • Db 815 APTVLGRCGSKKEPEPVLAQNMFLRIVYSDNSVQRGFQASH 856

RESULT 8
 A39288
 dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A39288
 R;Shimell, M. J.; Ferguson, E. L.; Childs, S. R.; O'Connor, M. B.
 Cell 67, 469-481, 1991
 A;Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
 A;Reference number: A39288; MUID:92034970; PMID:1840509
 A;Accession: A39288
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1057 <SH1>
 C;Genetics:
 C;Accession: FlyBase:tld
 C;Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeat
 C;Keywords: duplication; hydrolase; metalloproteinase; zinc
 F;136-329-/Domain: astacin homology <AST>
 F;352-464-/Domain: C1r/C1s repeat homology <C1R1>
 F;468-578-/Domain: C1r/C1s repeat homology <C1R2>
 F;585-620-/Domain: EGF homology <EG1>
 F;624-740-/Domain: C1r/C1s repeat homology <C1R3>
 F;747-782-/Domain: EGF homology <EG2>
 F;900-1013-/Domain: C1r/C1s repeat homology <C1R4>
 F;221,225,231,280-/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;222-/Active site: Glu #status predicted

Query Match 25.2%; Score 217.5; DB 1; Length 1057;
 Best Local Similarity 38.4%; Pred. No. 5.6e-14; Mismatches 47; Indels 1; Gaps 1;
 Matches 43; Conservative 21; Mismatches 47; Indels 1; Gaps 1;

Qy 39 VQCGTWTWKAEGGIFTSPNPKVPPDRCIYIIEAAPQQCIELYFDEKYSIESTPSSWCKF 98
 • Db 466 VVGGDKLTKQPSISIIFPMDYMPKRECWRITAPDNHQVALK-QSPEERKHDGAY 524

Qy 99 DHLERDGFPGFSPGSPGFRGFCQONPVKQSSGRFLWIKFADGELES 550
 • Db 525 DFEVRDGNHSRSLRIGRCGDKKUPNKTNSQMYIRFVSDSSVQKGSA 576

development protein tolkin (EC 3.4.24.-) - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
 C;Accession: S58984
 R;Finelli, A.-L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
 Genetics 141, 271-281, 1995
 A;Title: The tolkin gene is a toolloid/BMP-1 homologue that is essential for *Drosophila* development
 A;Reference number: S58984; MUID:96042912; PMID:8536976
 A;Accession: S58984
 A;Molecule type: mRNA
 A;Residues: 1-1464 <FTN>
 A;Cross-references: EMBL:U34777; NID:9102995; PIDN:AAQ47015.1; PID:91002986
 A;Note: the authors did not translate the codon for residue 722
 C;Genetics:
 A;Gene: tolkin
 A;Cross-references: FlyBase:FBgn004885
 C;Superfamily: astacin homology; EGF homology
 C;Keywords: hydrolase; metalloprotease; zinc
 F;529-722/Domain: astacin homology <AST>
 F;958-999/Domain: EGF homology <EGF>
 F;1118-1153/Domain: EGF homology <EGF1>
 F;614-618-624-673/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;615/Active site: Glu #status predicted
 Query Match 25.1%; Score 216.5; DB 2; Length 1464;
 Best Local Similarity 41.0%; Pred. No. 1e-13; 37; Mismatches 1; Gaps 1;
 Matches 41; Conservative 21; Indels 1; Gaps 1;
 QY 51 GIFTSPNVIKYKPPRECIVTEAARPROCIELYFDEKYSIESTPWECKFDHIEYRDCPPGF 110
 DB 851 GRLESPPNVIKYKPPRECIVTEAARPROCIELYFDEKYSIESTPWECKFDHIEYRDCPPGF 909
 QY 111 SPIIGRFFCQQNPPVIKSSGRFLWIKFFADGELESNGFSA 150
 DB 910 APLIGVFCGKYKPPNMKSSNSMYKFKVSDTSVQAGFSA 949
 .
 RESULT 10
 BMHU1
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
 N;Alternate names: bone morphogenic protein 1 (BMP1)
 C;Species: Homo sapiens (man)
 C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C;Accession: A37278; E58788
 R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsick, L.M.; Whitters, M.J.; Kriz, R.W.; Hew, Science 242, 1528-1534, 1988
 A;Title: Novel regulators of bone formation: molecular clones and activities.
 A;Reference number: A37278; MUID:89072730; PMID:3201241
 A;Accession: A37278
 A;Molecule type: mRNA
 A;Residues: 1-1730 <WOZ>
 A;Cross-references: GB:M22488; NID:9179499; PIDN:AAA51833.1; PID:9179500
 C;Genetics:
 A;Gene: GDB:BMP1
 A;Cross-references: GDB:125203; OMIM:112264
 A;Map position: 8p21-8p21
 C;Function:
 C;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type I;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; F1-2/2-Domain: signal sequence #status predicted <SIG>
 F;23-130/Domain: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
 F;332-431/Domain: C1r/C1s repeat homology <C1R1>
 F;435-544/Domain: C1r/C1s repeat homology <C1R2>
 F;551-587/Domain: EGF homology <EGF>
 F;591-700/Domain: C1r/C1s repeat homology <C1R3>
 R;911-142,332-363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;163-319,185-205,312-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F;213-223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F;214/Active site: Glu #status predicted

Query Match 24 5%; Score 211; DB 1; Length 730;
 Best Local Similarity 39.3%; Pred. No. 1.7e-13;
 Matches 44; Conservative 19; Mismatches 47; Indels 2; Gaps 2;
 Mismatches 44; Conservative 19; Mismatches 47; Indels 2; Gaps 2;
 Qy 41 CGTWTWKAEGGIFTSPNPKYKPPDRCTYITEAMPROCTYFDEKYSIESPWECKFDH 100
 Db 435 CGGDKKKDYH1-QSPNPYDDYRPSKWCIMR1QNSEPHVGLTF-QSFIERHDESCAVDY 492
 Qy 101 IEVRGPGFGSPITRGFGCQNPPIVKSSGFLWIKFADGLEMGSFARY 152
 Db 493 LEVRDGHSESTTLIGRYCGYERKPDIDKSTSSLWLFVSDGSINKAGFAVN F 544

RESULT 11.

A58788 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
 N1 Alternative names: bone morphogenic protein splice form BMP-1/His
 C1 Species: Homo sapiens (man)
 C1 Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
 C1 Accession: A37278; A37278;
 R1 Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mirsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hev
 Science 242, 1528-1534, 1988
 A1 Title: Novel regulators of bone formation: molecular clones and activities.
 A1 Reference number: A37278; MUID:89072730; PMID:3201241
 A1 Accession: A37278
 A1 Molecule type: mRNA
 A1 Residues: 1-702; EKRPALQPPRGRPHOLKFVRVKRNRTEQ' <WOZ>
 A1 Cross-references: GB:M2248; NID:9179499; PIDN:AA51833.1; PID:9179500
 R1 Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J1 Biol. Chem. 269, 32572-32578, 1994
 A1 Title: Bone morphogenetic protein-1 and a mammalian toll-like homologue (mTld) are encod
 A1 Reference number: A58788; MUID:95096114; PMID:7798260
 A1 Accession: A58788
 A1 Molecule type: mRNA
 A1 Residues: 703-823 <TAK>
 A1 Cross-references: GB:L35278; NID:9619423; PIDN:AAC41703.1; PID:9619424
 C1 Genetics:
 C1 Gene: GDB:BMP1; BMP-1
 A1 Cross-references: GDB:125203; OMIM:112264
 A1 Map position: 8p21-8p21
 C1 Function:
 C1 Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen typ
 C1 Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;
 C1 Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g
 F1:322-431/Domain: signal sequence #stratus predicted <SIG>
 F1:330-321/Domain: astacin homology <AST>
 F1:322-431/Domain: C1r/C1s repeat homology <C1R>
 F1:435-544/Domain: C1r/C1s repeat homology <C1R>
 F1:551-567/Domain: EGF homology <EGF>
 F1:591-700/Domain: C1r/C1s repeat homology <C1R>
 F1:738-752/Region: histidine-rich
 F1:91-142,332-363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F1:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-6
 F1:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F1:214/Active site: Glu #status predicted
 F1:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Search completed: May 18, 2004, 18:24:52
Job time : 22 secs

Db 61 KYPDPRECIVTEAAPROCTLYFDEKYSIERSWECKFDHIEVRDGFPGFSPILGRFCGQ 120
 Qy 121 QNPPVIKSSGRFLWIKFFADGELESMGFSARYNFTP 158
 Db 121 QNPPVIKSSGRFLWIKFFADGELESMGFSARYNFTP 158

GENERAL INFORMATION:
 APPLICANT: Asbrook et al.
 TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
 FILE REFERENCE: 21402-347A

CURRENT APPLICATION NUMBER: US/10/138,588
 CURRENT FILING DATE: 2002-05-01
 PRIOR APPLICATION NUMBER: 60/288,395
 PRIOR FILING DATE: 2001-05-03
 PRIOR APPLICATION NUMBER: 60/308,901
 PRIOR FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: 60/313,388
 PRIOR FILING DATE: 2001-08-17
 PRIOR APPLICATION NUMBER: 60/324,757
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: 60/288,900
 PRIOR FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 203

SEQ ID NO 30
 LENGTH: 526
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-138-588-38

RESULT 3
 Query Match 98.7%; Score 851; DB 13; Length 533;
 Best Local Similarity 100.0%; Pred. No. 3.4e-85; Mismatches 0; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 2, Application US/10041406
 Publication No. US20020164705A1
 GENERAL INFORMATION:
 APPLICANT: Meyers, Rachel
 APPLICANT: Gluckmann, Maria Alexandra
 APPLICANT: Curtis, Rory A.J.
 APPLICANT: Kapeller-Libermann, Rosana
 APPLICANT: Bandaru, Rajasekhar
 APPLICANT: Leiby, Kevin R.
 TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
 FILE REFERENCE: 10448-189001
 CURRENT APPLICATION NUMBER: US/10/162,435
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: US 09/836,499
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: PCT/US01/12420
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: US 60/197,507
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/891,008
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: PCT/US01/19963
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: US 60/214,220
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 09/860,868
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: PCT/US01/16013
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/205,674
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/886,429
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: PCT/US01/20055
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/213,963
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 10/041,406
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: PCT/US02/00275
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/260,286
 PRIOR FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: US 09/934,269
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: PCT/US01/41811
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/226,612
 PRIOR FILING DATE: 2000-08-21
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 27
 LENGTH: 533
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-041-406-2

RESULT 4
 Query Match 98.7%; Score 851; DB 13; Length 533;
 Best Local Similarity 100.0%; Pred. No. 3.4e-85; Mismatches 0; Indels 0; Gaps 0;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 27, Application US/10162435
 Publication No. US20030096305A1
 GENERAL INFORMATION:
 APPLICANT: Meyers, Rachel
 APPLICANT: Gluckmann, Maria Alexandra
 APPLICANT: Curtis, Rory A.J.
 APPLICANT: Kapeller-Libermann, Rosana
 APPLICANT: Bandaru, Rajasekhar
 APPLICANT: Leiby, Kevin R.
 TITLE OF INVENTION: NOVEL HUMAN MEMBRANE-ASSOCIATED PROTEIN AND
 FILE REFERENCE: 10448-189001
 CURRENT APPLICATION NUMBER: US/10/162,435
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: US 09/836,499
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: PCT/US01/12420
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: US 60/197,507
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/891,008
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: PCT/US01/19963
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: US 60/214,220
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 09/860,868
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: PCT/US01/16013
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/205,674
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/886,429
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: PCT/US01/20055
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/213,963
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 10/041,406
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: PCT/US02/00275
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/260,286
 PRIOR FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: US 09/934,269
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: PCT/US01/41811
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/226,612
 PRIOR FILING DATE: 2000-08-21
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 27
 LENGTH: 533
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-041-406-2

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-162-435-27

Query Match 98.7%; Score 851; DB 14; Length 533;
Best Local Similarity 100.0%; Pred. No. 3.4e-85; Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; LENGTH: 141

Qy 1 MTHGRSVHHLVAVASLILHSGATKKGKBEQTTSETQKSVQCGTWKHAEGGIFTSPNYP 60
Db 1 MTHGRSVHHLVAVASLILHSGATKKGKBEQTTSETQKSVQCGTWKHAEGGIFTSPNYP 60

Qy 61 KPPDRECIYIEBAAPROCIYFDEKYSIESWECKHIEVDRDGPGFSPNIGRCQ 120
Db 61 KPPDRECIYIEBAAPROCIYFDEKYSIESWECKHIEVDRDGPGFSPNIGRCQ 120

Qy 121 QNPPIVKSGRFPIKFGDGELESMSGRSARNTFP 156
Db 121 QNPPIVKSGRFPIKFGDGELESMSGRSARNTFP 156

RESULT 5

US-09-764-853-653

; Sequence 653, Application US/09764853

; Patent No. US2002009672A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PIZ06

; CURRENT APPLICATION NUMBER: US/09/764,853

; CURRENT FILING DATE: 2001-01-17

; PRIORITY: application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 939

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 653

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-764-853-653

Query Match 55.6%; Score 479; DB 9; Length 130;
Best Local Similarity 66.1%; Pred. No. 7.6e-45; Matches 80; Conservative 21; Mismatches 20; Indels 0; Gaps 0;
; LENGTH: 130

Qy 38 SVQCGTWKHAEGGIFTSPNYPSKYPDRECIYIEBAAPROCIYFDEKYSIESWECK 97
Db 9 ATQCGIHWRTSNGHGFASPNYPDSYSPNPKECIYIEBAAPROCIYFDEKYSIESWECK 68

Qy 98 FDHIEVRDGPGFSPNIGRCQWQNPPIVKSGRFPIKFGDGELESMSGRSARNTFP 157
Db 69 FDHIEVRDGPGFSPNIGRCQWQNPPIVKSGRFPIKFGDGELESMSGRSARNTFP 128

Qy 158 K 158
Db 129 K 129

RESULT 7

US-09-764-881-116

; Sequence 116, Application US/09764881

; Publication No. US2002008683A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PIZ207

; CURRENT APPLICATION NUMBER: US/09/764,881

; CURRENT FILING DATE: 2001-01-17

; PRIORITY: application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 192

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 116

; LENGTH: 141

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-764-881-116

Query Match 55.6%; Score 479; DB 12; Length 141;
Best Local Similarity 66.1%; Pred. No. 8.4e-45; Matches 80; Conservative 21; Mismatches 20; Indels 0; Gaps 0;
; LENGTH: 141

Qy 38 SVQCGTWKHAEGGIFTSPNYPSKYPDRECIYIEBAAPROCIYFDEKYSIESWECK 97
Db 9 ATQCGIHWRTSNGHGFASPNYPDSYSPNPKECIYIEBAAPROCIYFDEKYSIESWECK 68

Qy 98 FDHIEVRDGPGFSPNIGRCQWQNPPIVKSGRFPIKFGDGELESMSGRSARNTFP 157
Db 69 FDHIEVRDGPGFSPNIGRCQWQNPPIVKSGRFPIKFGDGELESMSGRSARNTFP 128

Qy 158 K 158
Db 129 K 129

RESULT 8

US-10-242-747-116

; Sequence 116, Application US/10242747

; Publication No. US2004000557A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PIZ07C1

; CURRENT APPLICATION NUMBER: US/10/242,747

; CURRENT FILING DATE: 2002-09-13

; PRIORITY: application number: 09/764,881

; PRIORITY FILING DATE: 2001-01-17

; PRIORITY APPLICATION NUMBER: 60/179,065

; PRIORITY FILING DATE: 2000-01-31

; PRIORITY APPLICATION NUMBER: 60/180,628

; PRIORITY FILING DATE: 2000-02-04

; PRIORITY APPLICATION NUMBER: 60/214,886

; LENGTH: 141

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-242-747-116

```

PRIORITY APPLICATION NUMBER: 60/217,487
PRIORITY FILING DATE: 2000-06-28
PRIORITY APPLICATION NUMBER: 60/225,758
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/220,963
PRIORITY FILING DATE: 2000-07-26
PRIORITY APPLICATION NUMBER: 60/217,496
PRIORITY FILING DATE: 2000-07-11
PRIORITY APPLICATION NUMBER: 60/225,447
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/218,290
PRIORITY FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or Palm.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 116
LENGTH: 141
TYPE: PRT
ORGANISM: Homo sapiens
; US-10-242-747-116

RESULT 9
Query Match 55.6%; Score 479; DB 15; Length 141;
Best Local Similarity 66.1%; Pred. No. 8.4e-45;
Matches 80; Conservative 21; Mismatches 20; Indels 0; Gaps 0;
QY 38 SVOCGTTWTKHAEGGFTSPNPKYPDPRECIVIYEADPROCYIYFDEKYSFESWEC 97
Db 9 ATQCGIWRITSNGHFAASPNNPDSYPPNKECIVYLEAFAQRQIETFDHYIIRSPEC 68
QY 98 FDHIEVRQPGFGSPPIGSPCGQONPPVWPKSSGFLWTFKPADGELESMGPSA 157
Db 69 FDHIEVRQPGFGSPPLIDRYCGVKSPPLIRSTGRMMWIKSSDDELEGIFRAKYSP 128
QY 158 K 158
Db 129 K 129

; US-10-276-774-2238
; Sequence 2238, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2238
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-276-774-2238

RESULT 9
Query Match 54.5%; Score 470; DB 12; Length 525;
Best Local Similarity 54.9%; Pred. No. 4.4e-43;
Matches 94; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
QY 6 SVLHI--VASLILHLSGATKKGKFKQTSETQKSVOCGTTWTKHAEGGFTSPNPKYP 63
Db 8 SVLKVLLITLVVLEGIAVQAQKTDQGQMGIGKHPATOCGIVWRITSNGHFAASPNNPDSY 67
QY 64 PDKCIVIYEADPROCYIYFDEKYSFESWEC 123
Db 68 PDKCIVIYEADPROFELTFDHYIYEPSFCRFDHLERDQPGFGSPPLIDRYCGVKSP 127
QY 124 PVTKSSGRFLWKFADGELESMGFSARYNFTP 156
Db 128 PLRSTGRMMWIKSSDDELEGIFRAKYSP 160

; US-10-147-493-114
; Sequence 114, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeJong, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filavoff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watarabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEAR
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33301C1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 114
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-147-493-114

RESULT 11
Query Match 54.5%; Score 470; DB 12; Length 352;
Best Local Similarity 53.9%; Pred. No. 2.6e-43;
Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
QY 6 SVLHI--VASLILHLSGATKKGKFKQTSETQKSVOCGTTWTKHAEGGFTSPNPKYP 63
Db 28 SVLKVLLITLVVLEGIAVQAQKTDQGQMGIGKHPATOCGIVWRITSNGHFAASPNNPDSY 87
QY 64 PDKCIVIYEADPROCYIYFDEKYSFESWEC 123
Db 88 PDKCIVIYEADPROFELTFDHYIYEPSFCRFDHLERDQPGFGSPPLIDRYCGVKSP 147

```

APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanae, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C252

CURRENT APPLICATION NUMBER: US/10/145,127

CURRENT FILING DATE: 2002-05-13

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 114

LENGTH: 525

TYPE: PRT

ORGANISM: Homo Sapien

US-10-145-127-114

RESULT 12

Query Match 54.5%; Score 470; DB 12; Length 525;
 Best Local Similarity 54.9%; Pred. No. 4-4e-43;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 1;

Qy 6 SVLHII--VSLVLIHLSSGATKKGTEKQTTSETOKSVQCGTWTHAEGGFTSPNYPKYP 63
 Db 8 SVLKVLLITLVVVEGIAVAKQTQDGQNGIKHHPATQCGIIVWRVNRNGHFAEPNYPDSYP 67

Qy 64 PDRDCIYIEAARPCICLYDEKYSIIPSWECKFDHIEVRDGFPGFSPILGRFCGQNP 123
 Db 68 PNKECIIYIEAAPRQIETFDHYIETPSFECRFDHLERVDRGPGFSPILDRYCVKSP 127

Qy 124 PVIKSSGRPLWIKFFADGELESMGFSARVNFTP 156
 Db 128 PLIRSTGRENWMKFSDEELEGIGFRAKYSFIP 160

RESULT 13

US-10-143-118-114

Sequence 114, Application US/10143118

Publication No. US2004004038335A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Godowski, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanae, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C228

CURRENT APPLICATION NUMBER: US/10/143,118

CURRENT FILING DATE: 2002-05-09

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 114

LENGTH: 525

TYPE: PRT

ORGANISM: Homo Sapien

US-10-143-118-114

RESULT 14

US-10-144-993-114

Sequence 114, Application US/10144993

Publication No. US20040038336A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Bersini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Stewart, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Tumas, Daniel
 APPLICANT: Watansabe, Colin K.
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3330R1C261
 CURRENT APPLICATION NUMBER: US/10/144,993
 CURRENT FILING DATE: 2002-05-13
 PRIOR APPLICATION removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO: 114
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-144-993-114
 Query Match 54.5%; Score 470; DB 12; Length 525;
 Best Local Similarity 54.9%; Pred. No. 4 4e-43;
 Matches 84; Conservative 29; Mismatches 38; Indels 2; Gaps 0
 2Y
 Db 6 SVLH-I-VASLILHLSGATRKKGTEKQPTSETQSKVSGGIVWTKHAE3GIFTSPNYPKVP
 8 SVLKVLVLTIVLWVGGIAVQKTOPGQNIQIKHIPATOCGIWVTSNGGHFASPNYPDSY
 64 PDEBCIVYIIEAARQCLIEYFDEKISIERSWEKEDHIVDRDPFGFSIIGPGCGQNP
 68 PNKECIVYIIEAARQRLIEFTDEHYIIPSFECRQFDHLEVRDGPFGFSPLIDRYCGVKSP
 QY 124 PVKSSGRLWIKPAGDELGELMSMGSARVNFTP 156
 128 PLRISIGRPMWIKSSDDELGIGFRAKISFIP 160
 Db

RESULT 15

US-10-158-787-114
 ; Sequence 114, Application US/10158787
 Publication No. US20040039164A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bersini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
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 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
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 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3330R1C449
 CURRENT APPLICATION NUMBER: US/10/158,787
 CURRENT FILING DATE: 2003-04-03

Query Match	54.5%	Score 470;	DB 12;	Length 525;
Best Local Similarity	54.9%	Pred. No. 4	4e-43;	
Matches	84;	Conservative	29;	Mismatches 2; Indels 1; Gaps 1;
Qy	6 SVHII--VASLTILHLSGATKGKTEKQTSETQKWSVQGTWTKHAEQGIFTSPNYPKSYP	63		
Db	8 SIVKLVITLVNVEGIAVAKQTKPQDGQNGIKHIPATQCGIWRTSNGHFASPNYPDSYP	67		
Qy	64 PDRCTYIITEAAPRCQTYIIFDKEYSIEPSWECCKFDHIEVRDQGPFGSPIIGRFGCQONP	123		
Db	68 PNKCTCYIITEAAPRQRIELTFDHYIYEPSFECRDPDILEVRDQGPFGSPLIDRYGVKSP	127		
Qy	124 PVIKSGEPLWITPFADGQBLIEUNGFSARYNFTP	156		
Db	128 PLIRSTGPRMWMKESDDELEGIGFRAKYSFIP	160		